(ix) FEATURE: (A) NAME/KEY: other (B) LOCATION: 3094 (C) MDENTIFICATION METHOD: blastn (D) OTHER INFORMATION: identity 98 region 165 id H75454 est	
<pre>(ix) FEATURE: (A) NAME/KEY: sig_peptide (B) LOCATION: 230307 (C) IDENTIFICATION METHOD: Von Heijne matrix (D) OTHER INFORMATION: score 4.9</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:	
AASTTSSAAG TIGTAGIGIT GITGITTICA GCCIGCIGCI GCIGCIGCIA TIGCGGCIAS	60
GGGAACCGTC GTGGGGAAGG ATGGTGTGCG AAAAATGTGA AAAGAAACTT GGTACTGTTA	12)
TCACTCCAGA TACATGGAAA GATGGTGCTA GGAATACCAC AGAAAGTGGT GGAAGAAAGC	180
TGAATGAAAA TAAAGCTTTG RCTTCAAAAA AAGCCAGAAT TGAWCCATA ATG GAA GAA Met Glu Glu -25	238
WTA AGT KCT CCA CTT GTA GAA TTT GTA AAA GTT TTG TGC ACC AAC CAG Xaa Ser Xaa Pro Leu Val Glu Phe Val Lys Val Leu Cys Thr Asn Gln -20 -15 -10	286
GTT CTC ATT ACT GCC AGG GCT GTG CCT ACA AAA AAG GCA TCT GTG CGA Val Leu Ile Thr Ala Arg Ala Val Pro Thr Lys Lys Ala Ser Val Arg -5 1 5	334
TGT GTG GMA AAA AGG TTT TGG ATA CCA AAA ACT ACA AGC AAA CAT CTG Cys Val Xaa Lys Arg Phe Trp Ile Pro Lys Thr Thr Ser Lys His Leu 10 25	382
TCT AGA TGT ATT GAT GGA ATT TCT GGC TTT CTA AAT GAT TTT ACT TTC Ser Arg Cys Ile Asp Gly Ile Ser Gly Phe Leu Asn Asp Phe Thr Phe 30 35 40	430
130 CTT GAA TTT TCA AGG CAT AGA TGT Tyo Leu 310 Phe Ser Arg His Arg Cys	45,

(L) INFORMATION FOR SEQ ID NO: 224:

4.5

GEQUENCE CHARACTERISTICS:

(A) LENGTH: 372 base pairs
a mappe Magnetic both

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: other (B) LOCATION: 125..367

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99

region 119..361

id AA242967

est

(ix) FEATURE:

(A) NAME/KEY: other (B) LOCATION: 6..125

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97

region 1..120 id AA242967

est

(ix) FEATURE:

(A) NAME/KEY: other (B) LOCATION: 125..261

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96

region 124..260

id C18969

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 2..125

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 95

region 2..125 id C18969

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 253..311

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96

region 251..309

id C18969

est

(1x) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 125..367

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99

region 101..343

id N40141

est

(ix) FEATURE:

(A) NAME/KEY: other

- (B) LOCATION: 24..125
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: .identity 97

region 1..102 id N40141 est

345

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 125..329
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 122..326

id R78319

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 9..125
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 7..123

id R78319

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (3) LOCATION: complement (125..367)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 112..354

id N27018

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (3) LOCATION: complement (73..125)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94

region 353..405

id N27018

est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 106..156
- (C) IDENTIFICATION METHOD: Von Haijne mairix
- (D) OTHER INFORMATION: score 4.8

seq LXXVVAFVAPGES/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

ATTOTTECT GGCCAGGCTC TOTGCTGACT CAAGTTCTTC AGTTCACGAT CTTCTAGTTT

MAGIYATBAD TEDACEASTG AGATCAAGAT C**CAGAGGAAG** AGGAG ATG GTC AGG WYW 117

-10

-5

1

GAA CCA CCA ACT GAC AAT CAG GAT ATT GAA CCT GGA CAA GAG AGA GAA Glu Pro Pro Thr Asp Asn Gln Asp Ile Glu Pro Gly Gln Glu Arg Glu 10 GGA ACA CCT CCG ATC GAA GAA CGT AAA GTA GAA GGT GAT TGC CAG GAA 261 Gly Thr Pro Pro Ile Glu Glu Arg Lys Val Glu Gly Asp Cys Gln Glu 25 ATG GAT CTG GAA AAG ACT CGG AGT GAG CGT GGA GAT GGC TCT GAT GTA 309 Met Asp Leu Glu Lys Thr Arg Ser Glu Arg Gly Asp Gly Ser Asp Val AAA GAG AAG ACT CCA CCT AAT CVT AAG CAT GCT AAG ACT AAA GAA GCA 357 Lys Glu Lys Thr Pro Pro Asn Xaa Lys His Ala Lys Thr Lys Glu Ala 60 GGA GAT GGG CCA TTG 372 Gly Asp Gly Pro Leu 70

(2) INFORMATION FOR SEQ ID NO: 225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 299..454
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 273..433

id AA100750

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 160..308
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 133..286

id AA100750

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24...159
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 1..136 id AA100750 .est

(ix) FEATURE:

- (A) NAME/KEY: other (B) LOCATION: 9..355
- (3) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 1..347 id N68686

est

(1K) FEATURE:

- (A) NAME/KEY: other(B) LOCATION: 355..402
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 348..395

1d N68686

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 400..429
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96

region 394..423

id N68686

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1...241
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90

region 5..245

id H24263

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 239..337
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95

region 244..342

id H24253

est

(1x) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 13...123
- .D. IDENTIFICATION METHOD: Von Heijne matrix
- 0) OTHER INFORMATION: score 4.8

seq PIVRLLSCEGTVA/KD

The opinional phaotistaton, one to be ob-

	-35		-30		-25
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CTG Leu	TGT Cys	GCC Ala	CGG Arg	AGA Arg -20	AGA Arg	ACT Thr	CGA Arg	GTC Val	CAG Gln -15	CGG Arg	CCT Pro	ATC Ile	GTC Val	AGG Arg -10	CTT Leu	99
TTG Leu	AGT Ser	TGC Cys	CCA Pro -5	GGA Gly	ACT Thr	GTG Val	GCC Ala	AAA Lys 1	GAC Asp	CTT Leu	AGG Arg	AGA Arg 5	GAC Asp	GAG Glu	CAG Gln	147
CCT Pro	TCA Ser 10	GGG Gly	AGC Ser	GTG Val	GAG Glu	ACA Thr 15	GGC Gly	TTT Phe	GAA Glu	GAC Asp	AAG Lys 20	ATT Ile	CCC Pro	AAA Lys	AGG Arg	195
AGA Arg 25	TTC Phe	TCG Ser	GAG Glu	ATG Met	CAA Gln 30	AAT Asn	GAA Glu	AGA Arg	CGA Arg	GAA Glu 35	CAG Gln	GCA Ala	CAG Gln	CGG Arg	ACT Thr 40	243
GTT Val	TTA Leu	ATA Ile	CAT His	TGC Cys 45	CCA Pro	GAG Glu	AAA Lys	ATC Ile	AGT Ser 50	GAA Glu	AAC Asn	AAG Lys	TTT Phe	CKK Xaa 55	AAA Lys	291
TAT Tyr	TTA Leu	TCC Ser	CAA Gln 60	TTT Phe	GGA Gly	CCT Pro	ATT Ile	AAT Asn 65	AAT Asn	CAT His	TTC Phe	TTC Phe	TAT Tyr 70	GAA Glu	AGC Ser	339
TTT Phe	GGT Gly	CTC Leu 75	TAT Tyr	GCT Ala	GTC Val	GTA Val	GAA Glu 80	TTT Phe	TGC Cys	CAA Gln	AAG Lys	GAA Glu 85	AGC Ser	ATA Ile	GGT Gly	387
TCA Ser	CTG Leu	CAG Gln	AAT Asn	GGG Gly	ACT Thr	CAT His	ACT Thr	CCA Pro	AGC Ser	ACG Thr	GCC Ala	ATG Met	GAG Glu	ACT Thr	GCA Ala	435

90 95 100 ATT CCA TTC AGA TCA CGT TCT TCA 459 Ile Pro Phe Arg Ser Arg Ser Ser

(2) INFORMATION FOR SEQ ID NO: 226:

(i) SEQUENCE CHARACTERISTICS:

110

- (A) LENGTH: 329 base pairs
- (3) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(1%) FEATURE:

105

- (A: NAME/KEY: other
- (B) LOCATION: 109..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95 region 43..253 id AA017309

	e	est
(1x) FEATURE	:	
(A) NAN	ME/KEY: other	
(B) LO	CATION: 93124	
(C) IDE	ENTIFICATION METHOD	: blastn
TO (C)	HER INFORMATION: i	dentity 96
	r	egion 2859

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(126..250)
- (I) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 1..125 id T52392

id AA017309

est

est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 21..200
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8

seq LVILSLKSQTLDA/ET

(X1) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

AGTAAGTCCC (TG CCG CCG GGC C al Pro Pro Gly Lo -55	
		AAC CGC AGC GCA Asn Arg Ser Ala	
		TGC ATT GCA GCT Cys Ile Ala Ala -20	
		AAG AGC CAA ACC Lys Ser Gln Thr -5	
		TAS AGO AAT CAC Tyr Ser Ash His 13	
		AAA CAS STT GAG Lys Gln Val Glu	
	TTG ARA AAD AT Leu Xaa Ash Mer Bs		329

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 385 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 39..385
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 97

region 1..347 id AA023764

est

- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 146..385
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 95

region 145..384

id C03036

est

- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 11..80
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 98

region 2..71

id C03036

est

- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 39..231
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 99

region 1..193

id R08519

est

- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 232..302
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 94

region 193..263

id R08519

est

- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: 11..109

- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8 seq SLVHLLCQNQVLG/NP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

AAGTSGCAAG			AAG GTA CTG (Lys Val Leu ' -25	
			CAT CTC CTA His Leu Leu -10	n
			GGC TGC TCA Gly Cys Ser	
	Asp Tyr	y Thr Pro	GAA GAG AAG Glu Glu Lys 25	
			GGC AGT GCC Gly Ser Ala 40	
			GTA AAT GGT Val Asn Gly 55	a
			CAA AAM TTG Gln Xaa Leu	
			CCA ACT GGA Pro Thr Gly	

(2) INFORMATION FOR SEQ ID NO: 228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- 101 TOPOLOGY: LINEAR
- .ii MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
- 1% FEATURE:
 - TO MAMERIEU E ERABE

id R19497 est

(ix) FEATURE:

- (A) NAME/KEY: other
 (B) LOCATION: 236..270
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 219..253

id R19497

est

(ix) FEATURE:

- (A) NAME/KEY: other(B) LOCATION: 54..238
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96

region 1..185

id H75597

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 236..270
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 184..218

id H75597

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..238
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 1..179

id H93398

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 236..270
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 178..212

id H93398

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 98..270
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 1..173

id HUM030E11B

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..127
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98 region 118..244 id AA280273 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 50..142

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.8

seg WAFSCGTWLPSRA/EW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

GCGTCCGCGC CATCAGGCCC GAGATAGCGG CGAGGTCCGC TTTCAGTGT ATG GTT TTC 58 Met Val Phe -30 GCT GCC AAA CGG TTC TGC TTG GTG CCA TCC ATG GAG GGC GTG CGC TGG 106 Pro Ala Lys Arg Phe Cys Leu Val Pro Ser Met Glu Gly Val Arg Trp GCC TIT TOO THO GRO ACT THE CITY COG AGO CHA GOO HAA THE CITY CITY 154 Ala Pne Ser Cys Gly Thr Trp Leu Pro Ser Arg Ala Glu Trp Leu Leu -10 -5 RCA GTG CGA TCG ATT CAS CCC GAG GAG AAG GAG CGC ATT GGC CAG TTC 202 Kaa Val Arg Ser Ile Gln Pro Glu Glu Lys Glu Arg Ile Gly Gln Phe 10 GTC TTT GCC CGG GAC GCT AAG GCA GCC ATG GCT GGT CGT CTG ATG ATA Val Phe Ala Arg Asp Ala Lys Ala Ala Met Ala Gly Arg Leu Met Ile 25 30 AGG AAA TTA GTT GCA GAG AAT CGA 274 Arg Lys Leu Val Ala Glu Asn Arg 40

. . . .

(2) INFORMATION FOR SEQ ID NO: 229:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRAMDEDMESS: DOUBLE

TOPOLOGY: LINEAR

ALE' MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Surrenals

L. FEATURE.

id HSC13B041 est

(ix) FEATURE:

- (A) NAME/KEY: other
 (B) LOCATION: 2..99
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 18..115 id HSC13B041

est

(ix) FEATURE:

- (A) NAME/KEY: other(B) LOCATION: 90..208
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 71..189 id T08849

est

(ix) FEATURE:

- (A) NAME/KEY: other
 (B) LOCATION: 19..99
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 1..81 id T08849

est

(ix) FEATURE:

- (A) NAME/KEY: other
 (B) LOCATION: 19..101
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 1..83 id H88132

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LCCATION: 90..158
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92

region 71..139

id H88132

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LCCATION: 153..208
- (C) ICENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 140..130

id H88132

est

(1K) FEATURE:

- (A) NAME/KEY: other
 (B) LCCATION: 111..208
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100 region 92..189 id T33149 est (in) FEATURE: (A) NAME/KEY: other (B) LOCATION: 19..110 (C) IDENTIFICATION METHOD: blastn (D) OTHER INFORMATION: identity 97 region 1..92 id T33149 est (ix) FEATURE: (A) NAME/KEY: other (B) LOCATION: 18..99 (C) IDENTIFICATION METHOD: blastn (D) OTHER INFORMATION: identity 98 region 1..82 id AA121114 est (ix) FEATURE: (A) NAME/KEY: other (B) LOCATION: 158..196 (C) IDENTIFICATION METHOD: blastn (D) OTHER INFORMATION: identity 100 region 141..179 id AA121114 est (ix) FEATURE: (A) NAME/KEY: sig_peptide (B) LOCATION: 12..89 (C) IDENTIFICATION METHOD: Von Heijne matrix (D) OTHER INFORMATION: score 4.7 seq LIMQLGSVLLTRC/PF (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229: ACTITICCAA G ATG GCG TCG AAG ATA GGT TCG AGA CGG TGG ATG TTG CAG Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln -25 OTS ATS ATS CAS TIG GGT TOS GIG CIG CIC ACA CGS ISC COS IIIT IGG Low Ile Mot Glm Leu Gly Ser Val Leu Leu Thr Ang Gys Bio Ene Trp 330 T30 TTC AGC CAG CTC ATG CTG TAC GCT GAG AGG GCT GAG GCA CGC Gly Cyp Phe Ser Sin Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg CORRESPONDED AND COA CTG COT TAC CTG TAT THE RAW AND COSC GCA Arg Lyp Pro Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala

(2) INFORMATION FOR SEQ ID NO: 230:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 301 base pairs (B) TYPE: NUCLEIC ACID (C) STRANDEDNESS: DOUBLE (D) TOPOLOGY: LINEAR 	
(ii) MOLECULE TYPE: CDNA	
<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo Sapiens (F) TISSUE TYPE: Brain</pre>	
(ix) FEATURE: (A) NAME/KEY: other (B) LOCATION: 40293 (C) IDENTIFICATION METHOD: blastn (D) OTHER INFORMATION: identity 95 region 19272 id W52056 est	
<pre>(ix) FEATURE: (A) NAME/KEY: sig_peptide (B) LOCATION: 128220 (C) IDENTIFICATION METHOD: Von Heijne matrix (D) OTHER INFORMATION: score 4.7</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:	
AAGAACTGCG TCTCGCGACC CAGGCGCGGG TTCCCGGAGG ACAGCCAACA AGCGATGCTG	60
CCGCCGCCGT TTCCTGATTG GTTGTGGGTG GCTACCTCTT CGTTGTGATT GGCCGCTAGT	120
GAGCAAG ATG CTG AGC AAG GGT CTG AAG CGG AAA CGG GAG GAG GAG GAG Met Leu Ser Lys Gly Leu Lys Arg Lys Arg Glu Glu Glu -30 -25 -20	169
GAG AAG GAA COT CTG GCA GTC GAO TCC TGG TGG CTA GAT CCT GGC CAC Glu Lys Glu Pro Leu Ala Val Asp Ser Trp Trp Leu Asp Pro Gly His -15	217
GCA GCG GTG GCA CAG GCA CCC CCG GCC GTG GCC TCT AGC TCC CTC TTT Ala Ala Val Ala Gln Ala Pro Pro Ala Val Ala Ser Ser Ser Leu Phe 1 5 10 15	265
GAC CTC TCA GT3 CTC AAG CTC CAC CAC AGC CGC GGG Asp Leu Ser Val Leu Lys Leu His His Ser Arg Gly	301

(2) INFORMATION FOR SEQ ID NO: 231:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: CDNA

(v1) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 93..282
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 88..277

id **W**02951

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 40..93
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 36..89

id W02951

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 347..381
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 345..379

id W02951

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (E) LOCATION: 7..41
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 2..36

id W02951

est

fix: FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 316..347
- (C) IDENTIFICATION METHOD: blastm
- (D) OTHER INFORMATION: identity 1)()

region 313...344

id W02951

est

(D) OTHER INFORMATION: identity 94

region 279..312

id W02951

est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 93..305

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100

region 81..293

id N40687

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 12..93

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98

region 1..82 id N40687

est

(ix) FEATURE:

(A) NAME/KEY: other(B) LOCATION: 305..381

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100

region 292..363

id N40687

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 93..305

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100

region 80..292

id N44829

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 305..381

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100

region 291..367

id N44828

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 40..93

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98

region 28..81

id N44828

est

(ix) FEATURE:

(A) NAME/KEY: other

- (B) LOCATION: 93..381
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: .identity 99

region 79..367

id R91018

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 14..93
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 1..80 id R91018

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 93..305
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 80..292

id W19557

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 13..93
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96

region 1..81

id W19557

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 305..380
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 201..366

id W19557

est

(1x) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 282..329
- (C) IDENTIFICATION METHOD: Von Heighe matrix
- (D) OTHER INFORMATION: score 4.7

seq SLAAALTLHGHWG/LG

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 831:

AAGGAACGAG ATGGCGGTTC TOTGGAGGCT GAGTGCCGTT TOCGGTGCCC TAGGAGGCCG 60

AGCTCTGTTG DTTCGAACTC CAGTGGTCAG AMCCTGCTCA TATCTCAGGA TTTCTTCAGG 120

TGGGTCTGCT TCCGGCTGCT TATTTGAATC CTTGCTCTGC G ATG GAC TAT TCC CTG 296

Met Asp Tyr Ser Leu
-15

GCT GCA GCC CTC ACT CTT CAT GGT CAC TGG GGC CTT GGA CAA GTT GTT

Ala Ala Ala Leu Thr Leu His Gly His Trp Gly Leu Gly Gln Val Val

-10

-5

1

5

ACT GAC TAT GTT CAT GGG GAT GCC TTG CAG AAA GCT
Thr Asp Tyr Val His Gly Asp Ala Leu Gln Lys Ala
10 15

(2) INFORMATION FOR SEQ ID NO: 232:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 444 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 138..348
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 97 region 123..338 id HUM090D04B

est

- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 10..143
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 94

region 1..134 id HUM080D04B

est

- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 348..408
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 98

region 339..399 id HUM080D04B

est

- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 407..445
 - (C) IDENTIFICATION METHOD: blast::
 - (D) OTHER INFORMATION: identity 94

region 397..435 id HUMO80D04B est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 138..274
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96

region 127..263

id H29248

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 11..143
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94

region 1..133 id H29248

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 273..348
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 263..338

id H29248

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 348..387
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 339..378

id H29248

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 382..411
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93

region 354..403

id H29315

est

in FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 138..348
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 103..338 id HUM179H02B

non-

- (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 - region 1..134 id HUM179H02B est

(ix) FEATURE:

- (A) NAME/KEY: other
 (B) LOCATION: 348..397
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 339..388 id HUM179H02B

est

(ix) FEATURE:

- (A) NAME/KEY: other(B) LOCATION: 407..437
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 396..426 id HUM179H02B

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 138..299
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95

region 135..296

id H73551

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 3..143
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94

region 1..141

id H73551

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 292..348
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93

region 290..346

id H73551

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 402..441
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 407..446

id H73551

est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 138..326
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96

region 94..282 id W68502

est

(ix) FEATURE:

(A) NAME/KEY: other(B) LOCATION: 44..143

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..100

region 1..100 id W68502

est

(ix) FEATURE:

(A) NAME/KEY: other(B) LOCATION: 348..408

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98

region 306..366 id W68502

est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 181..396

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.7

seq LSLXASYIFGISG/FE

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

AGTITICAGG ARATTIGGAA GCTGCCGCAG TAGTIGGAGT CTAAGGACTC GTGACAATCT	60
TOGGGTGOOD TTCGAGAGAA AAGGGGAGGA TGCCACTGGA GTCATCCTCT TCAATGCCAC	120
TATCCTTCCC ATCTBYBYTD RCCCTCRGTA CCACACATA CTAACCCTTC CCCTNCTCTG	180
ATG TCT TAC ATC ACC TCC CAG GAG ATG AAG TGT ATT CTT CAC TGG TTT Met Ser Tyr Ile Thr Ser Gln Glu Met Lys Cys Ile Leu His Trp Phe -70 -65	228
GOC AAT TGG TCA GGT CCC CAG CGT GAA CGT TTC CTA GAG GAC CTG GTA Ala Aan Trp Ser Gly Pro Gln Arg Glu Arg Phe Leu Glu Asp Leu Val -%50 -45	276
GOT ARG GOA GTG CCA GAA AAA TTA CAA CCA HTG CTG GAT AGT CTG GAG Ala Lys Ala Val Pro Glu Lys Leu Gln Pro Xaa Leu Asp Ser Leu Glu -40 -35 -30 -25	324
CAG CIT AGT GTG TCT GGG GCA GAC GAC CAG CIT CTA TCT TTG WGT GCC Glm Let Ser Val Ser Gly Ala Asp Asp His Let Let Ser Let Xaa Ala	372

CGC AAT GAA TTT GTC AGA CAG TCG Arg Asn Glu Phe Val Arg Gln Ser 10

444

(2) INFORMATION FOR SEQ ID NO: 233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 46..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 6..366 id W31798

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 2..353

id AA056667

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 68..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 4..342

id AA131958

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 35..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 1..334

1d H10262

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 77..406
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99 region 1..330 id W95790 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 200..427

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.7

seq LIVYLWVVSFIAS/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

AAGACGAGGT CATGAATCAT GTGACGGTGG CTTGAGGAGG AACCTGTCTT TAAAGCTGTC	60										
COTGAAGTGA CAGCGGAGAG AACCAGGCAG CCCAGAAACC CCAGGCGTGG AGATTGATCC	120										
TGCGAGAGAA GGGGGTTCAT CATGGCGGAT GACCTAAAGC GATTCTTGTA TAAAAAGTTA	180										
CCAAGTGTTG AAGGGCTCC ATG CCA TTG TTG TGT CAG ATA GAG ATG GAG TAC Met Pro Leu Leu Cys Gln Ile Glu Met Glu Tyr -75											
CTG TTA TTA AAG TGG CAA ATG ACA ATG CTC CAG AGC ATG CTT TGC GAC Leu Leu Lys Trp Gln Met Thr Met Leu Gln Ser Met Leu Cys Asp -65 -50	280										
CTG GTT TCT TAT CCA CTT TTG CCC TTG CAA CAG ACC AAG GAA GCA AAC Leu Val Ser Tyr Pro Leu Leu Pro Leu Gln Gln Thr Lys Glu Ala Asn -45 -40 -35	328										
TTG GAC TTT CCA AAA ATA AAA GTA TCA TCT GTT ACT ATA ACA CCT ACC Leu Asp Phe Pro Lys Ile Lys Val Ser Ser Val Thr Ile Thr Pro Thr -30 -25	376										
AGG TGG TTC MAT TTA ATC GTT TAC CTT TGG GTG GTG AGT TTC ATA GCC Arg Trp Pne Xaa Leu Ile Val Tyr Leu Trp Val Val Ser Phe Ile Ala -15	424										
AGC AGE AGT Ser Ser 1	433										

TR' INFÓRMATION FOR SEQ ID NO: 234:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

HE MÜLECULE TYPEH CONA

(ix) FEATURE:

- (A) NAME/KEY: other(B) LOCATION: 18..158
- (C) IDENTIFICATION METHOD: blastn (D) OTHER INFORMATION: identity 92

region 39..179 id C15963

est

(ix) FEATURE:

- (A) NAME/KEY: other(B) LOCATION: 139..239
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 161..261

id C15963

est

(ix) FEATURE:

- (A) NAME/KEY: other(B) LOCATION: 17..219
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 22..224

id W07092

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..239)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 140..377

id W72958

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..239
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 18..255

id W24219

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LCCATION: 2..239
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 16..253 id AA040714

est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LCCATION: 45...110
- (C) ICENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7

seq SVMGVCLLIPGLA/TA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

AAAGGACCCA GAAGTAGGGT TTTGGCCTAG GTAACGGGGC AGAG ATG TGG TTC GAG Met Trp Phe Glu ATT DIC COC GGA CTC TCC GTC ATG GGC GTG TGC TTG TTG ATT CCA GGA Ile Leu Pro Gly Leu Ser Val Met Gly Val Cys Leu Leu Ile Pro Gly -15CTS GCT ACT GCG TAC ATC CAC ARG TTC ACT AAC CGG GGC AAG GAA AAA 152 Leu Ala Thr Ala Tyr Ile His Xaa Phe Thr Asn Arg Gly Lys Glu Lys 1 AGS GTT GCT CAT TTT GGG TAT CAC TGG AGT CTG ATG GAA AGA GAT AGG 200 Arg Val Ala His Phe Gly Tyr His Trp Ser Leu Met Glu Arg Asp Arg 20 CGC ATC TCT GGA GTT GAT CGT TAC TAT GTG TCA AAG GGT CCA GGG 245 Arg Ile Ser Gly Val Asp Arg Tyr Tyr Val Ser Lys Gly Pro Gly 35

(2) INFORMATION FOR SEO ID NO: 235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Prostate

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 204..351
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93

region 162..309

id AA017973

est

:ix: FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 204..351
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93 region 181..328 id AA021972

est

(D) OTHER INFORMATION:	region 181328 id AA013987 est
<pre>(ix) FEATURE: (A) NAME/KEY: other (B) LOCATION: 204351 (C) IDENTIFICATION METHOM (D) OTHER INFORMATION:</pre>	OD: blastn identity 93 region 168315 id AA014054 est
<pre>(ix) FEATURE: (A) NAME/KEY: other (B) LOCATION: 204351 (C) IDENTIFICATION METHO (D) OTHER INFORMATION:</pre>	
<pre>(ix) FEATURE: (A) NAME/KEY: sig_peptic (B) LOCATION: 205342 (C) IDENTIFICATION METHO (D) OTHER INFORMATION:</pre>	DD: Von Heijne matrix
(xi) SEQUENCE DESCRIPTION: SEQ	Q ID NO: 235:
AGTTTAGCGA CCGGACCCGA AACGGGGAAG TTC	GTCTTGTG TGGAGAGGTT AGTAAAGCAG 60
CGCGCGCGTC ACCAGAGTCG TTTCTCTTCG GAC	GTCTTAGG TGATCGAGGG TGTGCCCAGG 120
GGGCGGACTT GTTTGCGCCT CCCGTTCCCT CCC	CAATTICC AAACGIGICA CCCCGGCGCC 180
GACGGCCCTG TGCAGGGGAA GCAG ATG GAG 1 Met Glu F -45	TTC AAG CTG GAG GCT CAT CGC 231 Phe Lys Leu Glu Ala His Arg -40
ATC GTC AGC ATC TCT CTG GGC AAG ATC Ile Val Ser Ile Ser Leu Gly Lys Ile -35	TAC AAC TCG CGG GTC CAG CGC 279 Tyr Asn Ser Arg Val Gln Arg -25
GGC GGC ATC AAG CTG CAT AAG AAC CTC Gly Gly Ile Lys Leu His Lys Asn Leu -20	CTG GTC TCG CTG GTG CTG CGC 327 Leu Val Ser Leu Val Leu Arg -10
ASG CCC GCC AAG TCT ACC CGA GCG GGG Xaa Pro Ala Lys Ser Thr Arg Ala Gly -5	354
(2) INFORMATION FOR ORD TRUE	

(2) INFORMATION FOR SEQ ID NO: 236:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 420 base pairs

- (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR
- (11) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
- (ix) FEATURE:
 - (A) NAME/KEY: other
 (B) LOCATION: 37..215
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 97

region 1..179 id AA146876

est

- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 214..368
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 98

region 179..333 id AA146876

est

- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 370..399
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 100

region 334..363

id AA146876

est

- (1x) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 49..319
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 99

region 15..285

1d AA044109

est

- (1x) FEATURE:
 - TA: NAME/KEY: other
 - (P) LOCATION: 371..414
 - (0) IDENTIFICATION METHOD: blastn
 - [0] OTHER INFORMATION: identity 100

region 338..381

id AA044109

est

- (ix) FEATURE:
 - == +p.wm/v=v+ ++ ...

id AA044109 est

(ix) FEATURE:

- (A) NAME/KEY: other (B) LOCATION: 52..362
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 27..337 id H21138

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 372..407
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 347..382

id H21138

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..254
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 14..216

id AA150025

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 307..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 271..332

id AA150025

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 253..315
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92

region 216..278

id AA150025

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 370..414
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 332..376

1d AA150025

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 59..368
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98 region 1..310 id N28828 est

(ix) FEATURE:

(A) NAME/KEY: other(B) LOCATION: 370..414

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100

region 311..355

id N28828

est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 94..384

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.6

seq IASGLGLXLDCWT/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

AATCTAGCCC CGCCCCAGGC GAGGGCGCCG CACCCACACC GCGCTGCGCA GTTTTGTTCT 60 GCTCCAGCTG TTCGAAGGTG ATCCAGACGC AAG ATG GCT GTC CTC TCT AAG GAA Met Ala Val Leu Ser Lys Glu -95 TAT GGT TIT GTG CTT CTA ACT GGT GCC AGC TIT ATA ATG GTG GCC Tyr Gly Phe Val Leu Leu Thr Gly Ala Ala Ser Phe Ile Met Val Ala -90 CAC CTA GCC ATC AAT GTT TCC AAG GCC CGC AAG AAG TAC AAA GTG GAG His Leu Ala Ile Asn Val Ser Lys Ala Arg Lys Lys Tyr Lys Val Glu THE CCT HIS ARE THE AGE AGE GAS CCT GAR ART GGG CHE HIS TIC AAC Tyr Pro Ile Met Tyr Ser Thr Asp Pro Glu Asn Gly His Ile Phe Asn -55 TGC ATT CAG CGA GCC CAC CAG AAC ACG TTG GAA GTG TAT CCT CSC TTC Cys Ile Gln Arg Ala His Gln Asn Thr Leu Glu Val Tyr Pro Xaa Phe TTA TTT TTT STA GOT GTT GGA GGT GTT TAC CAC CCG CGT ATA GCT TCT Led Phe Fre Led Ala Val Gly Gly Val Tyr His Pro Arm Ile Ala Ser -25 GUC CTG GII TTO DON CTG GAT TGT TGG ACG AGT TOT TTA TGO TTA TGG Gly Leu Gly Leu Xaa Leu Asp Cys Trp Thr Ser Ser Leu Cys Leu Trp -1)STA TTA SAR AGG STG GGG 420 Led Led B. Sly Pro Gly

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 28..227
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 1..200 id AA074804

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 265..310
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 238..283 id AA074804

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 227..263
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 201..237

id AA074804

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (3) LOCATION: 352..385
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94

region 328..361

id AA074804

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (2) LOCATION: complement(259..408)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 123..272

1d N93600

est

(in FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(85..207)

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
. region 325..447
.id N93600

est.

(1x) FEATURE:

- (A) NAME/KEY: other
- (P) LOCATION: complement(202..408)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 117..323

id AA074748

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(116..153)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 375..412 id AA074748

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement (167..202)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 324..359 id AA074748

10 AAU/4/48

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(258..408)
- (C) IDENTIFICATION METHOD: blastn
- (E) OTHER INFORMATION: identity 99

region 123..273

1d N93603

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (P) LOCATION: complement(208..251)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 280..323

id N93603

est

(iii) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(163..202)
- IDENTIFICATION METHOD: blastn
- D) OTHER INFORMATION: identity 97

WO 99/06548		374	PCT/IB98
(3) (C)	NAME/KEY: other LOCATION: complement IDENTIFICATION MET OTHER INFORMATION:	HOD: blastn	
(B) (C)	NAME/KEY: sig_pept: LOCATION: 272397	HOD: Von Heijne matr	
(xi) SEQU	ENCE DESCRIPTION: SI	EQ ID NO: 237:	
AAAAGGAAAG AGGT	YSGGAG CGCTCGCGAG A	ICTCGGACC ACCCAACCTG	AAAGGTGCTT 60
AGGAAGTTGA AAGG	CCCAGA GGAGGCCTCC GG	GGCAAATGG CCGGAGCTGG	ACCGACCATG 120
CTGCTACGAG AAGA	GAATGG CTGTTGCAGT CO	GGCGTCAGA GCAGCTCCAG	TGCCGGGGAT 180
TCGGACGGAG AGCG	CGAGGA CTCGGCGGCT GA	AGCGCGCCC GACAGCAGCT	AGAGGCGCTG 240
CTCAACAAGA CTAT	GCGCAT TCGCATGACA G	ATG GAC GGA CAC TGG Met Asp Gly His Trp -40	
GCT TTC TCT GCA Ala Phe Ser Ala -35	CTG ACC GTG ACT GCA Leu Thr Val Thr Ala -30	A ATG TCA TCC TGG GC A Met Ser Ser Trp Al -25	T CGG CGC 340 a Arg Arg -20
AGG AGT TOO TOA Arg Ser Ser Ser	AGC CGT CGG ATT CCT Ser Arg Arg Ile Pro -15	TCT CTG CCG GGG AG Ser Leu Pro Gly Se -10	C CCC GTG 388 r Pro Val -5
TGC TGG GCC TGG Cys Trp Ala Trp			406
(2) INFORMATION	FOR SEQ ID NO: 238:		
(A) (B) (C)	NCE CHARACTERISTICS: LENGTH: 208 base pa TYPE: MUCLEIC ACID STRANDEDNESS: DOUBL TOPOLOGY: LINEAR	irs	
ASSA MOTO	THE MUDE. COME		

(2) INFORMA

- (i) S
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM. Homo Sapiens
 (F) TISSUE TYPE: Liver
- (ix) FEATURE:

- (A) NAME/KET: other
- (B) LOCATION: 56..207

(C) IDENTIFICATION METHOD: blastn

			(D)	OTH	ER I	NFOR	MAT I	ON:	reg	ion :	20	171				
	()	iw)	(B)	NAMI LOCA I DEI	E/KE ATION NTIF: ER IN	N: 6	92 ION 1	METH	ider reg:	ntity	y 97 38:	176				
			(B) (C) (D)	NAMI LOCA I DEN	E/KEY ATION NTIF: ER IN	1: 56 [CAT] IFORN	510 ION N	O3 METHO ON:	D: \ scor seq	e 4. RLLI	. 5 LRRFI	LASVI	atri: IS/RE			
	(:	(1)	SE QUI	ENCE	DESC	JRIP'	LION	: SE(2 ID	NO:	238.	:				
ACT	rgac <i>i</i>	AGG	CAGG	GAGG	GC T	AGGC'	rgtg(C AT	CCT	CCGC	TCG	CATT	GCA (GGGA	G ATG Met	58
			CTT Leu													106
AAG Lys	CCC Pro	TCT Ser	CAG Gln 5	GGT Gly	CAG Gln	TGG Trp	CCA Pro	CCC Pro 10	CTC Leu	ACT Thr	TCC Ser	AGA Arg	GCC Ala 15	CTG Leu	CAG Gln	154
ACC Thr	CCA Pro	CAA Gln 20	TGC Cys	AGT Ser	CCT Pro	GGT Gly	GGC Gly 25	CTG Leu	ACT Thr	GTA Val	ACA Thr	CCC Pro 30	AAC Asn	CCA Pro	GCC Ala	202
	ACG Thr 35															208
(2)	INFK)RMA	TION	FOR	SEQ	io t	4:0 : - 1	239:								
			(B)	LENC TYPE STRE TOPO	STH: E: NI ANDEE DLOGE	400 JOLEI INESS	base C AC S: DC	e pai CID OUBLE								

างราวร**ทุธ**ป ตากกระ

- (A) NAME/KEY: other
- (B) LOCATION: 124..343
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 103..322

id H72703

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..135
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 4..115

id H72703

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 357..398
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 336..377

id H72703

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 7..343
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 1..337

id W68324

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 357..391
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 351..385

id W68324

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 7..134
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95

region 1..128

id AA054941

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 191..283
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 185..277

id AA054941

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..191
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92

region 117..184

id AA054941

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 361..398
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92

region 360..397

id AA054941

est

(1X) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..343
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 97..316

id AA128297

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..134
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 1..108

id AA128297

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 357..398
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 330..371

id AA128297

est

DIM! FEATURE:

- (A) NAME/KEY: other
- (E) LOCATION: complement(153..300)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95

region 108..255

1d H72704

est

1 M FEATURE:

The STANE COURSE SEARCH

id H72704 est

ſ	iх	FEATURE:	
١	T .	L LIGHT ONE.	

(A) NAME/KEY: other

(B) LOCATION: complement(101..151)

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98

region 259..309

id H72704

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: complement(357..398)

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 95

region 9..50 id H72704

est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 311..385

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.5

seq FLLLLEVSHLLLI/IN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

AGACGTGTTC TTCCGGTGGC GGASGGCGGA TTAGCCTTCG CGGGGCAAAA TGGAGCTCGA GGCCATGAGC AGATATACCA GCCCAGTGAA CCCAGCTGTC TTCCCCCCATC TGACCGTGGT 120 GCTTTTGGCC ATTGGCATGT TCTTCACCGC CTGGTTCTTC GTTTACGAGG TCACCTCTAC 180 CAAGTACACT CGTGATATCT ATAAAGAGCT CCTCATCTCC TTAGTGGCCT CACTCTTCAT 240 GGGCTTTGGA GTCCTCTTCC TGCTGCTCTG GGTTGGCATC TACGTGTGAG CACCCAAGGG 300 TAACAACCAG ATG GCT TCA CTG AAA CCT GCT TTT GTA AAT TAC TTT TTT 349 Met Ala Ser Leu Lys Pro Ala Phe Val Asn Tyr Phe Phe -20 TTA CTG TTG CTG GAA GTG TCC CAC CTG CTG CTC ATA ATA AAT GCA GAA Leu Leu Leu Glu Val Ser His Leu Leu Leu Ile Ile Asn Ala Glu -10 --5 GGG 400 Gly 5

(2) INFORMATION FOR SEQ ID NO: 240:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 395 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

(A) NAME/KEY: other(B) LOCATION: 226..396

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100

region 202..372

id N40054

est

(1x) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 27..162

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 94

region 2..137

1d N40054

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 158..214

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100

region 134..190

id N40054

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 15..146

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98

region 2..133

id W25433

est

(ix) FEATURE:

(A) NAME/KET: other

(B) LOCATION: 226..305

(T) IDENTIFICATION METHOD: blastn

TD, OTHER INFORMATION: identity 98

region 213..292

id W25483

est

(ix' FEATURE:

AR MANR/KEL: other

B 180ATION, 157..214

TO THE PROPERTY OF THE PROPERT

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 34..157
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 1..124 id C17967

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 226..324
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 194..292

id C17967

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 157..214
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 125..182

id C17967

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 326..387
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95

region 293..354

id C17967

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 226..396
- (C) IDENTIFICATION METHOD: blastn
- (E) OTHER INFORMATION: identity 100

region 167..337

id N27721

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (E) LOCATION: 61..162
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96

region 1..102

id N27721

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 158..214
- (C) IDENTIFICATION METHOD: blastn
- (D. OTHER INFORMATION: identity 100 region 99..155

id N27721 est

(1x) FEATURE:		
	1	CCATIOC.

(A) NAME/KEY: other

(B) LOCATION: 50..214

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99

region 1..165 id T47061

est

(ix) FEATURE:

(A) NAME/KEY: other(B) LOCATION: 226..377

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99

region 177..328

id T47061

est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 156..386

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.5

seq LFWVIVLTSWITI/FQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

AAAAACGTCC ATAACTGAAA GTAGCTAAGG CACCCCAGCC GGAGGAAGTG AGCTCTCCTG	60
GGGCGTGGTT GTTCGTGATC CTTGCATCTG TTACTTAGGG TCAAGGCTTG GGTCTTGCCC	120
C3CAGACCCT T3GGACGACC CGGCCCCAGC GCAST ATG AAC CTG GAG CGA GTG Met Asn Leu Glu Arg Val -75	173
TOO AAT GAG GAG AAA TTG AAC CTG TGC CGG AAG TAC TAC CTG GGG GGG Ser Asn Glu Glu Lys Leu Asn Leu Cys Arg Lys Tyr Tyr Leu Gly Gly -70 -65 -60	221
TTT GCT TTC CTG CCT TTT CTC TGG TTG GTC AAC ATC TTC TGG TTC TTC Phe Ala Phe Leu Pro Phe Leu Trp Leu Val Asn Ile Phe Trp Phe Phe -55 -40	269
GGA GAG GGG TIV KITT GTC CCA GCC TAC ACA GAA CAG AGC CAA ATC AAA Arm Hiu Ala Pow Deu Val Pro Ala Tyr Thr Glu Gin Ser Gin He Lys -35 -30 -25	317
GGC TAT GTC TGG UGC TCA GCT GTG GGC TTC CTC TTC TGG GTG ATA GTG Gly Tyr Val Trp Arg Ser Ala Val Gly Phe Leu Phe Trp Val Ile Val -20 -10	365
GTU AGO TOU TOU ATO AGO ATO TTO CAG ATO Leu Tor Ger Tro lle Tor Ile Phe Glo Ile	395

(2) INFORMATION FOR SEQ ID NO: 241:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 189 base pairs (B) TYPE: NUCLEIC ACID (C) STRANDEDNESS: DOUBLE (D) TOPOLOGY: LINEAR	
(ii) MOLECULE TYPE: CDNA	
<pre>(vi) OPIGINAL SOURCE: (A) ORGANISM: Homo Sapiens (F) TISSUE TYPE: Lung (cells)</pre>	
<pre>(ix) FEATURE: (A) NAME/KEY: other (B) LOCATION: 80115 (C) IDENTIFICATION METHOD: blastn (D) OTHER INFORMATION: identity 100</pre>	
<pre>(ix) FEATURE: (A) NAME/KEY: sig_peptide (B) LOCATION: 73135 (C) IDENTIFICATION METHOD: Von Heijne matrix (D) OTHER INFORMATION: score 4.4</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:	
ATTTTTTTCT TGCTCGTGGG CTCGGACGAG TACGGAGCGC CTGCAGGGAC AGCCTGGAT	A 60
AAGGCTCACT TG ATG GCT CAG TTG GGA GCA GTT GTG GCT GTG GCT TCC AG Met Ala Gln Leu Gly Ala Val Val Ala Val Ala Ser Se -20 -15 -10	T 111
TTC TTT TGT GCA TCT CTC TTC TCA GCT GTG CAC AAG ATA GAA GAG GGA Phe Phe Cys Ala Ser Leu Phe Ser Ala Val His Lys Ile Glu Glu Gly -5 1 5	159
CAT ATT GGG GTA TAT TAC AGA GGC GGT GTG His Ile Gly Val Tyr Tyr Arg Gly Gly Val 10 15	189
(2) INFORMATION FOR SEQ ID NO: 242:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 313 base pairs (E) TYPE: NUCLEIC ACID (C) STRANDEDNESS: DOUBLE (D) TOPOLOGY: LINEAR	
(ii) MOLECULE TYPE: CDNA	
(vi) ORIGINAL SOURCE:	

(A) DRGANISM: Homo Sapiens

- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 62..308
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95

region 16..262

id AA044042

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 46..78
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90

region 1..33

id AA044042

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 75..308
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 9"

region 6..239

id AA127902

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (5) LOCATION: 93..308
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 1..216

id AA056679

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(104..308)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 246..450

id W93399

est

is Elerure

- A NAME/KEY: other
- TB: LOCATION: 126..308
- 407 IDENTIFICATION METHOD: blastn
- O OTHER INFORMATION: identity 97

region 2..184 id H39528

est

(D)	OTHER	INFORMATION:	score 4.4
			seq LVFMVPLVGLIHL/GW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

GCGAAGGTTG TCGGGATCCG CGGCAGCAGC GGCTGCTTGA GATCTGTTTC TGGGGCCTCT	60
GGCGGTGGCG GCCTGGGGCG GCGCGACGGC TGGTGCGCAG GTACACTGAT GCTGAAGTAC	120
T ATG AGC CTT CGG AAC TTG TGG AGA GAC TAC AAA GTT TTG GTT TTT ATG Met Ser Leu Arg Asn Leu Trp Arg Asp Tyr Lys Val Leu Val Phe Met -25 -10	169
GTC CCT TTA GTT GGG CTC ATA CAT TTG GGG TGG TAC AGA ATC AAA AGC Val Pro Leu Val Gly Leu Ile His Leu Gly Trp Tyr Arg Ile Lys Ser -5	217
AGC CCT GTT TTC CAA ATA CCT AAA AAC GAC GAC ATT CCT GAG CAA GAT Ser Pro Val Phe Gln Ile Pro Lys Asn Asp Asp Ile Pro Glu Gln Asp 10 15 20	265
AGT CTG GGA CTT TCA AAT CTT CAG AAG AGC CAA ATC CAG GGG ATA CTG Ser Leu Gly Leu Ser Asn Leu Gln Lys Ser Gln Ile Gln Gly Ile Leu 25	313

(2) INFORMATION FOR SEQ ID NO: 243:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 415 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (71) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Spleen
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 57..306
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 99 region 33..232

id AA088487

est

- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: 341..409
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.4

seq VFCLLISIPTPSA/HL

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

AGTCGTTGCC	ATSGATCCTG	GGGACGACTG	GCTGGTGGAA	TCCTTGCGCT TGTAAATCGT	60
ACCAGGATTT	CTATGCATTC	GACCTGTCAG	GAGCCACTCG	AGTCCTTGAA TGGATTGATG	120
ACAAAGGAGT	CTTTGTTGCT	GGCTATGAAA	GCCTGAAAAA	GAATGAAATT CTTCATCTGA	180
AATTACCTCT	CAGACTTTCT	GTAAAGGAAA	ACAAGGGCTT	ATTCCCAGAA AGAGATTTCA	240
AAGTGCGCCA	TGGAGGATTT	TCAGACAGGT	CTATCTTTGA	TCTAAAGCAT GTGCCACATA	300
CCAGGTATGG	TCAATTTTGT	GATCCAGCCA		ATG GGA TGG GAT GGC Met Gly Trp Asp Gly -20	355
		al Phe Cys 1		TCC ATT CCC ACC CCC Ser Ile Pro Thr Pro -5	403
TCA GCA CAC Ser Ala His					415

(2) INFORMATION FOR SEQ ID NO: 244:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 458 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (VI) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (1x) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 156..451
 - (C) IDENTIFICATION METHOD: blastn
 - (C) OTHER INFORMATION: identity 99 region 122..417 id AA085629

est

ik PEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 44..144
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94 region 14..114 id AA085629

est

WO 99/06548 386 (D) OTHER INFORMATION: identity 99 region 134..237 id AA132309 est (ix) FEATURE: (A) NAME/KEY: other (B) LOCATION: 47..144 (C) IDENTIFICATION METHOD: blastn (D) OTHER INFORMATION: identity 95 region 29..126 id AA132309 est (ix) FEATURE: (A) NAME/KEY: other (B) LOCATION: 274..314 (C) IDENTIFICATION METHOD: blastn (D) OTHER INFORMATION: identity 100 region 254..294 id AA132309 est (ix) FEATURE: (A) NAME/KEY: other (B) LOCATION: 47..144 (C) IDENTIFICATION METHOD: blastn (D) OTHER INFORMATION: identity 92 region 15..112 id H35088 est (ix) FEATURE: (A) NAME/KEY: other (B) LOCATION: 156..345 (C) IDENTIFICATION METHOD: blastn (D) OTHER INFORMATION: identity 98 region 63..252 id HUML11153 est (ix) FEATURE: (A' NAME/KEY: sig_peptide (B) LOCATION: 12..365 (C) IDENTIFICATION METHOD: Von Heijne matrix (D) OTHER INFORMATION: score 4.4 seq ILAHRLGLIPIHA/DP (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244: AGAGATTGAA G ATG GCG GCT TCT CAG GCG GTG GAG GAA ATG CGG ACC GCG 50 Met Ala Ala Ser Gln Ala Val Glu Glu Met Arg Thr Ala -115 -110 TGG TTC TGG GGG AGT TTG GGG TTC GCA ATG TCC ATA CTA CTG ACT TTC 98 Trp Phe Trp Gly Ser Leu Gly Phe Ala Met Ser Ile Leu Leu Thr Phe

-95

-105

-100

CCG GTA ACT ACT CCG GTT ATG ATG ATG CCT GGG ACC AGG RMC GGY. TTC Pro Val Thr Ile Pro Val Met Met Pro Gly Thr Arg Xaa Gly Phe

-80 -85 -75

GRA Xaa		Phe						194
GA3 Glu								242
CGA Arg -40								290
GTG Val								338
CTG Leu								386
AAC Asn								434
CTC Leu 25								458

(2) INFORMATION FOR SEQ ID NO: 245:

(i: SEQUENCE CHARACTERISTICS:

(A) LENGTH: 383 base pairs

- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR
- (ii) MCLECULE TYPE: CDNA
- (V1) OFIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Muscle
- .m' FEATURE:
 - TAT NAME/KEY: other
 - (B* LOCATION: 61..188
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 97 region 45..172 id AA156837

id AA156837 est

(ix) FEATURE:

- (A) NAME/KEY: other(B) LOCATION: 189..256
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 172..239 id AA156837

est

(ix) FEATURE:

- (A) NAME/KEY: other(B) LOCATION: 16..64
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97 region 1..49

id AA156837

est

(ix) FEATURE:

- (A) NAME/KEY: other
 (B) LOCATION: 15..220
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 1..206 id AA196478

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 252..334
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90

region 236..318 id AA196478

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (3) LOCATION: 222..256
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 207..241

id AA196478

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..226
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95

region 44..209 id AA181144

est

(ix) FEATURE:

- (A) NAME/KEY: other
 (B) LOCATION: 252..334
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 90

region 235..317

. id AA181144

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 17..64
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 1..48

id AA181144

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 225..256
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96

region 209..240

id AA181144

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 185..334
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94

region 169..318

id AA228369

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..184
- (C) IDENTIFICATION METHOD: blastn
- (5) OTHER INFORMATION: identity 98

region 46..169

id AA228369

est

tam) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..64
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95

region 8..50

1d AA228369

est

11H FEATURE:

- (A) NAME/KEY: other
- (8) LOCATION: 15..219
- (T) IDENTIFICATION METHOD: blastn
- 'D' OTHER INFORMATION: identity 97

region 1..205

(B) LOCATION: 252..334

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: . identity 90

region 236..318

id W04828 est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 341..380

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100

region 323..362

id W04828

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 221..256

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97

region 206..241

id W04828

est

(ix) FEATURE:

(A) NAME/KEY: sig peptide

(B) LOCATION: 12..242

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.4

seq FEARIALLPLLQA/ET

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

ATA	CTGC	GAG '		a Sei			n Ası		G CCG Pro -65	50
	GGC Gly									98
	TCG Ser									146
	CAC His									194
	GAG Glu -15									242
	ACC Thr									29û
	GCC Ala									338

20

25

30

GHT GTT CCA CAC AAC CCG CTG GGT GCC CCC CTT GAT CGG GGA GCT

Xaa Val Pro His Asn Pro Leu Gly Ala Pro Leu Asp Arg Gly Ala

35 • 40 45

- (2) INFORMATION FOR SEQ ID NO: 246:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 310 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR
 - (11) MOLECULE TYPE: CDNA
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Lymph ganglia
 - (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 58..271
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 95 region 54..267 id AA027968

est

- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 105..289
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 92

region 94..278

id N90497

est

- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 10..108
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 95

region 1..99

id N90497

est

- ix FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 63..307
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 97

region 21..265

id HSC0SD021

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(C) IDENTIFICATION METHOD: blastn (D) OTHER INFORMATION: identity 95	
(ix) FEATURE: (A) NAME/KEY: other (B) LOCATION: 116274 (C) IDENTIFICATION METHOD: blastn (D) OTHER INFORMATION: identity 95 region 61219 id R38457 est	
<pre>(ix) FEATURE: (A) NAME/KEY: other (B) LOCATION: 55107 (C) IDENTIFICATION METHOD: blastn (D) OTHER INFORMATION: identity 98</pre>	
<pre>(ix) FEATURE: (A) NAME/KEY: other (B) LOCATION: 273307 (C) IDENTIFICATION METHOD: blastn (D) OTHER INFORMATION: identity 100</pre>	
<pre>(ix) FEATURE: (A) NAME/KEY: sig_peptide (B) LOCATION: 164289 (C) IDENTIFICATION METHOD: Von Heijne matrix (D) OTHER INFORMATION: score 4.4</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:	
AATGOGOGAC TGAGCCGGGT GGATGGTACT GCTGCATCCG GGTGTCTGGA GGCTGTGG	CC 60
STITITGTTTT CTTGGCTAAA ATCGGGGGAG TGAGGCGGGC CGGCGCGGCG	GG 120
CTCCGGAACC ACTGCACGAC GGGGCTGGAC TGACCTGAAA AAA ATG TCT GGA TTT Met Ser Gly Phe -40	175
CTA GAG GGC TTG AGA TGC TCA GAA TGC ATT GAC TGG GGG GAA AAG CGC Leu Glu Gly Leu Arg Cys Ser Glu Cys Ile Asp Trp Gly Glu Lys Arg -35 -30 -25	223
ART ACT ATT GCT TCC ATT GCT GCT GGT GTA CTA TTT TTT ACA GGC TGG Asn Thr Ile Ala Ser Ile Ala Ala Gly Val Leu Phe Phe Thr Gly Trp -20 -15 -10	271
IGG ATT ATC ATA GAT GCA GCT GTT ATT TAT CCC ACC CGG Irp lie lie Asp Ala Ala Val lie Tyr Pro Thr Arg	310

1 5

(2) INFORMATION FOR SEQ ID NO: 247:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 398 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 101..386
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 98 region 73..358 id AA133050

est

- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 71..100
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 96

region 42..71 id AA133050

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 168..313
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 145..290 1d AA159550

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 71..169
- O IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 47..145 id AA159550

est

ix FEATURE:

TA) NAME/KEY: other

(ix	}	FEATURE:	

- (A) NAME/KEY: other(B) LOCATION: 33..68
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91 region 10..45

id AA159550

es

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 225..356
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4

seq LVFLTFLSIPSFV/GL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

AAGGTGCTCG	TCATGCGC	AA TGTGGCGC1	rg cggc <mark>ggc</mark> gg	CAGGGCCTGT GTGTGCTGAG	60
GCGGCTGAGC	GGCGGACA	TG CACACCACA	AG AGCGTGGCGA	TGGAACAGTA ACCGGGCTTG	120
TGAGAGGGCT	CTGCAGTA	TA AACTAGGAC	SA CAAGATCCAT	GGATTCACCG TAAACCAGGT	180
GACATCTGTT	CCCGAGCT	GT TCCTGACTO	SC AGTGAAGCTC	ACCC ATG ATG ACA CAG Met Met Thr Gln	235
GAG CCA GG Glu Pro Gl -40	T ATT TAC y Ile Tyr	ACC TGG CCA Thr Trp Pro	GAG AAA ACA Glu Lys Thr -30	CGA ATA ATC TGT TCA Arg Ile Ile Cys Ser -25	284
		Pro Leu Pro		CTG GTG TTC CTC ACA Leu Val Phe Leu Thr -10	332
				AAT ATC CGT GCA GAG Asn Ile Arg Ala Glu 5	380
ACC TTT CT Thr Phe Le					398

(2) INFORMATION FOR SEQ ID NO: 248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (3) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement (53..194)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95

region 444..585

id AA161193

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(227..324)
- (C) IDENTIFICATION METHOD: blastn
- ([)) OTHER INFORMATION: identity 94

region 311..408

1d AA161193

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (E) LOCATION: complement(328..406)
- (I) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 230..308

id AA161193

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement (408..446)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92

region 188..226

id AA161193

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement (328..406)
- (C) IDENTIFICATION METHOD: blastn
- (I) OTHER INFORMATION: identity 97

region 75..153

id R06283

est

(1%, FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(275..324)
- (G) IDENTIFICATION METHOD: blastn
- (D. OTHER INFORMATION: identity 93

region 156..205

id R06283

est

in FEATURE:

'A NAME/KEY: other

id R06283

(ix) FEATURE:

- (A) NAME/KEY: other(B) LOCATION: 328..384
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 286..342 id AA152388

est

(ix) FEATURE:

- (A) NAME/KEY: other
 (B) LOCATION: 131..183
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96

region 89..141

id AA152388

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 283..324
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 242..283

id AA152388

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 42..85
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90

region 1..44

id AA152388

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 351..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96

region 312..367

id AA159107

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 408..445
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94

region 371..403

id AA159107

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 193..225
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93

region 166..198 _id AA159107 est (1x) FEATURE: (A) NAME/KEY: other (B) LOCATION: complement(171..324) (C) IDENTIFICATION METHOD: blastn (I) OTHER INFORMATION: identity 90 region 313..466 1d AA152366 est (ix) FEATURE: (A) NAME/KEY: other (B) LOCATION: complement (328. 406) (C) IDENTIFICATION METHOD: blastn (D) OTHER INFORMATION: identity 100 region 232..310 1d AA152366 (1K) FEATURE: (A) NAME/KEY: other (B) LOCATION: complement (408..446) (C) IDENTIFICATION METHOD: blastn (D) OTHER INFORMATION: identity 92 region 190..228 id AA152366 est (ix) FEATURE: (A) NAME/KEY: sig peptide (B) LOCATION: 39..80 (C) IDENTIFICATION METHOD: Von Heighe matrix (D) OTHER INFORMATION: score 4.4 seg FLTALLWRGRIPG/RQ (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248: ASCGGAGACG CAGAGTCTTG AGCAGCGCGN CAGGCACC ATG TTC CTG ACT GCG CTC Met Phe Leu Thr Ala Leu -10TTY TGG CGC GGC ATT CCC GGC CGT CAG TGG ATC GGG AAG CAC CGG 104 Lea Trp Arg Sly Arg Ile Pro Sly Arg Gln Trp Ile Sly Lys His Arg CGG CGG CGG TTC GTG TCG TTG CGC GGC AAG CAG AAC ATG ATC CGC CGC 152 Arg Pro Arg Phe Val Ser Leu Arg Ala Lys Gln Asn Met Ile Arg Arg 10 15 TTR GAG ATC GAG GOG GAG ARC CAT TAC TGG CTG AGC ATG CGC TAC ATG Dog 5ld Tie 3ld Ala Glu Ash His Tyr Trp Led Ser Met Pro Tyr Met

TTC Phe	GAG Glu	GCS Ala	ATA Ile 60	AAG Lys	GCG Ala	GCC Ala	GCC Ala	ACT Thr 65	TCC Ser	AAG Lys	TTC Phe	CCC Pro	CCG Pro 70	CAT His	AGA Arg	2	96
TTC Phe	ATT Ile	GCG Ala 75	GAC Asp	CAG Gln	CTC Leu	GAC Asp	CAT His 80	CTC Leu	AVK Xaa	VGT Xaa	CAC His	CAA Gln 85	GAA Glu	ATG Met	GTC Val	3	44
CTA Leu	ATC Ile 90	CTG Leu	AGT Ser	CGT Arg	CAC His	CCT Pro 95	TGG Trp	ATT Ile	TTA Leu	TGG Trp	ATC Ile 100	ACG Thr	GAG Glu	CTG Leu	ACC Thr	3	92
ATC Ile 105	TTT Phe	ACC Thr	TGG Trp	TCT Ser	GGA Gly 110	CTG Leu	AAA Lys	AAC Asn	TGT Cys	AGC Ser 115	TTG Leu	TGT Cys	GAA Glu	AAT Asn	GAG Glu 120	4	40
	TGG Trp															4 !	58

(2) INFORMATION FOR SEQ ID NO: 249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 20..400
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 1..391

id W56872

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..317
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 1..291

id W31727

est

(1X) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..375
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 1..354 id W16469 est

(1x) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 45..400

(\mathbb{C}) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99

region 1..356 id N31028

est

(1X) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 22..375

(\mathbb{C}) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98

region 1..354 id W16470

est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 120..389

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.3

seq TCLTACWTALCCC/CL

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

AACTTGCTCT GAGACAGGTG CGGCAAGTCT ACTGCGGGCT GGTCCGGGCT CCTCAGGTTC	60
AGACCCGACC GTTATCCAGT CGGTTCGTGG AGAGGAGAGG	119
ATG AAC CAA GAG AAC CCT CCA CCA TAT CCA GGC CCT GGT CCA ACG GCC Met Asn Glu Asn Pro Pro Pro Tyr Pro Gly Pro Gly Pro Thr Ala -90 -85 -85	167
CCA TAC CCA CCT TAT CCA CCA CAA CCA ATG GGT CCA GGA CHT ATG GGG Pro Tyr Pro Pro Tyr Pro Pro Gln Pro Met Gly Pro Gly Xaa Met Gly -70 -65 -60	215
GGA CCC TAC CCA CCT CCT CAA GGG TAC CCC TAC CAA GGA TAC CCA CAG Gly Pro Tyr Pro Pro Pro Gln Gly Tyr Pro Tyr Gln Gly Tyr Pro Gln -55 -50 -45	263
TAC GGC TGG CAG GGT GGA CCT CAG GAG CCT CCT ARA ACC ACA GTG TAT Tyr Gly Trp Gln Gly Gly Pro Gln Glu Pro Pro Lys Thr Thr Val Tyr -40 -35 -30	311
GTG GTA GAA GAC CAA AGA AGA GAT GAG CTA GGA CCA TCC AGC TGC CTC Val Val Glu Asp Gln Arg Arg Asp Glu Leu Gly Pro Ser Thr Cys Leu -25 -15	359
Soft now made Made Made does one whom was was was the	300

(2) INFORMATION FOR SEQ ID NO: 250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 56..332 id AA022276

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..57
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 4..59 id AA022276

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (3) LOCATION: 329..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95

region 329..368

id AA022276

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..284
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 44..273

id W87295

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 284..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 274..321

id W87295

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 12..57
- (\odot) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 2..47 id W87295 est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 329..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95

region 318..357

id W87295

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 68..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 1..264 id W01758

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 329..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95

region 261..300

id W01758

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95

region 50..249

ia W57829

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 12..58
- (I) IDENTIFICATION METHOD: blastn
- (2) OTHER INFORMATION: identity 100

region 3..49

id W57829

est

127 FEATURE:

- (A) NAME/KET: other
- 'R' LOCATION: 22..235

est

	(.	ix)	(A) (B) (C)	NAMI LOCA I DEI	E/KE ATION NTIFI ER IN	N: 1: ICAT:	ll' ION !	72 METHO	DD: '	re 4						
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:															
AAG'	TTCC	GCC I	ATG (Met <i>i</i>	GCC '	TCC ' Ser :	Leu (GAA (Glu ' -50	GTC Z	AGT (CGT A	Ser	CCT (Pro 1	CGC . Arg .	AGG ' Arg :	TCT Ser	49
CGG Arg	CGG Arg -40	GAG Glu	CTG Leu	GAA Glu	GTG Val	CGC Arg -35	AGT Ser	CCA Pro	CGA Arg	CAG Gln	AAC Asn -30	AAA Lys	CAT His	TCG Ser	GTG Val	97
CTT Leu -25	TTA Leu	CCT Pro	ACC Thr	TAC Tyr	AAC Asn -20	GAG Glu	CGC Arg	GAR Glu	GAA Glu	CTG Leu -15	CCG Pro	CTC Leu	ATC Ile	GTG Val	TGG Trp -10	145
CTG Leu	CTG Leu	GTG Val	AAA Lys	AGC Ser -5	TTC Phe	TCC Ser	GAG Glu	AGT Ser	GGA Gly 1	ATC Ile	AAC Asn	TAT Tyr	GAA Glu 5	ATT Ile	ATA Ile	193
					AGC Ser											241
TTG Leu	GAG Glu 25	AAG Lys	ATC Ile	TAT Tyr	GGG Gly	TCA Ser 30	GAC Asp	AGA Arg	ATT Ile	CTT Leu	CTA Leu 35	AGA Arg	CCA Pro	CGA Arg	GAG Glu	289
					GGA Gly 45											337
					CAT His											367
(2)	INFO	ORMAT	поі	FOR	SEQ	ID N	10: 2	251:								
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 407 base pairs (B) TYPE: NUCLEIC ACID (C) STRANDEDNESS: DOUBLE (D) TOPOLOGY: LINEAR 															
	(ii) MOLECULE TYPE: CDNA															

(ix) FEATURE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

- (A) NAME/KEY: other(B) LOCATION: 70..408
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 61..399 id AA114853

(ix) FEATURE:

- (A) NAME/KEY: other
 (B) LOCATION: 19..68
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 11..60 id AA114853

est

(ix) FEATURE:

- (A) NAME/KEY: other(B) LOCATION: 18..402
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 7..391 id W23545

est

(1x) FEATURE:

- (A) NAME/KEY: other
 (B) LOCATION: 70..409
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 42..381 id AA069652

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 28..68
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 1..41 id AA069652

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..343
- (0) IDENTIFICATION METHOD: blastn
- 3D) DTHER INFORMATION: identity 98

region 8..333

1d AA084987

est

(ix) FEATURE:

- (A) NAME/KEY: other 'B: LOCATION: 63..409
- o' IDENTIFICATION METHOD: blasts

(ix) FEATURE:

(ix) FEATURE:

(A) NAME/KEY: other (B) LOCATION: 8..38

(A) NAME/KEY: sig_peptide

(B) LOCATION: 303344 (C) IDENTIFICATION METHOD: Von Heijne matrix (D) OTHER INFORMATION: score 4.2 seq CPTCLCAPSXXWG/EP	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:	
ATCCGGTGCA CGCGAGTSTT CTGAAACGTC AGCTGCGCTC CCCTAGGAGT GCTGAGCCCG	60
CGGAACCGCA GCCATGACTG AGGCTGATGT GAATCCAAAG GYCTATCCCC TTGCCGATGC	120
CCACCTCACC AAGAAGCTAC TGGACCTCGT TCAGCAGTCA TGTAACTATA AGCAGCTTCG	180
GAAAGGWGCC AATGAGGCCA CCAAAACCCT CAACAGGGGC ATCTCTGAGT TCATCGTGAT	240
GGCTGCAGAC GCCGAGCCAC TGGAGATCAT TCTGCACCTG CCGCTGCTGT GTGAAGACAA	300
GA ATG TGC CCT ACG TGT TTG TGC GCT CCA AGC AVN SCC TGG GGA GAG Met Cys Pro Thr Cys Leu Cys Ala Pro Ser Xaa Xaa Trp Gly Glu -10 -5 1	347
CCT GTG GGG TCT CCA GGC CTG TCA TCG CCT GTT CTG TCA CCA TCA AAG Pro Val Gly Ser Pro Gly Leu Ser Ser Pro Val Leu Ser Pro Ser Lys 5 10 15	395
AAG GCT CGC AGC Lys Ala Arg Ser 20	407
(2) INFORMATION FOR SEQ ID NO: 252: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 168 base pairs (B) TYPE: NUCLEIC ACID (C) STRANDEDNESS: DOUBLE (D) TOPOLOGY: LINEAR	
(i1) MOLECULE TYPE: CDNA	
<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo Sapiens (F) TISSUE TYPE: Brain</pre>	
<pre>(ix) FEATURE: (A) NAME/KEY: other (B) LOCATION: 43163 (C) IDENTIFICATION METHOD: blastn (D) OTHER INFORMATION: identity 98</pre>	

		DD: blastn identity 100 region 131 id N52621 est	
(B) (C)	JRE: NAME/KEY: other LOCATION: 21168 IDENTIFICATION METHO OTHER INFORMATION:	DD: blastn identity 98 region 5152 id AA157163 est	
(B) (C)	NAME/KEY: sig_peption LOCATION: 1066 IDENTIFICATION METHO	de DD: Von Heijne matrix score 4.2 seq AVAASAASGQAEG/KK	
(xi) SEQUE	ENCE DESCRIPTION: SEC	Q ID NO: 252:	
		CG GTG GCA GCC TCG GCC GC La Val Ala Ala Ser Ala Al -10	
		GAT CTG CGG GTC ATC GAT Asp Leu Arg Val Ile Asp 5	
		GAC ATC ACC GGA GTC AAG Asp Ile Thr Gly Val Lys 25	
GTS CTC ATC TCC Val Leu Ile Ser 30			168
(2) INFORMATION	FOR SEQ ID NO: 253:		
(A) (B) (C)	CE CHARACTERISTICS: LENGTH: 433 base pai TYPE: NUCLEIC ACID STRANCEDNESS: DOUBLE TOPOLOGY: LINEAR		
(11) MOLEC	WLE TYPE: CDNA		
(A)	NAL SOURCE: CRGANISM: Homo Sapie DEVELOPMENTAL STAGE:		

- (ix) FEATURE:
 - (A) NAME/KEY: other
 (B) LOCATION: 37..139
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 97 region 1..103

id AA102280

est

est

- (ix) FEATURE:
 - (A) NAME/KEY: other(B) LOCATION: 340..433
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 97

region 304..397 id AA102280

est

- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 132..433
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 98

region 87..388

id R13711

est

- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 71..139
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 97

region 27..95

id R13711

est

- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 132..401
 - (C) IDENTIFICATION METHOD: blastn
 - (C) OTHER INFORMATION: identity 98

region 87..356

id R61022

est

- (ix) FEATURE:
 - (A) MAME/KEY: other
 - (E) LOCATION: 71..139
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 97

region 27..95

id R61022

est

(ix) FEATURE:

(B) LOCA	E/KEY: other ATION: 132389 NTIFICATION METHO CR INFORMATION:		
(B) LOCA	C/KEY: other ATION: 50139 HTIFICATION METHO CR INFORMATION:		
(B) LOCA		D: blastn identity 95 region 338384 id N44705 est	
(B) LOCA (C) IDEN		D: blastn identity 98 region 75382 id H29689 est	
(B) LOCA (C) IDEN (D) OTHE	R INFORMATION:	D: Von Heijne mat: score 4.2 seq SLLXRVSVTAVAA.	
ATTECTOCTG COCGTAGTA	AG OC ATG GOG GOO	: ATG AGT TTG TTG :	
TIG GTT ACT GG3 GTG Ger Val Thr Ala Val -5			
CTU GGA TTT GGG GGC Len Gly Pho Gly Gly 10			

433

(2) INFORMATION FOR SEQ ID NO: 254:

110

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 453 base pairs

CGT AAT TTC TAT GAT AGT CCT GMA AAG ATA TAT GAA AGA ACA ATG

Arg Asn Phe Tyr Asp Ser Pro Xaa Lys Ile Tyr Glu Arg Thr Met

- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Lymph ganglia
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 86..452
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 98

region 43..409

id W00599

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 54..96
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 12..54

id W00599

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 108..405
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 107..404

id AA088577

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..100
- [] IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94

region 29..96 id AA088577

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (5) LOCATION: 6..41
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91

region 1..36 id AA088577

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (E) LOCATION: 40..189
- (C) IDENTIFICATION METHOD: blastn
- (I) OTHER INFORMATION: identity 96 region 7..156

id R18030

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 188..311
- (C) IDENTIFICATION METHOD: blastn
- (0) OTHER INFORMATION: identity 98

region 156..279

id R18030

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 100..261
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 46..207

id H85485

est

las FENTURE:

- (A) NAME/KEY: sig_peptide
- (P) LOCATION: 61..135
- (3) IDENTIFICATION METHOD: Von Heijne matrix
- (I) OTHER INFORMATION: score 4.2

seq LDLLRGLPRVSLA/NL

MI DECUENCE DESCRIPTION: SEQ ID NO: 254:

(2) INFORMATION FOR SEQ ID NO: 255:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 425 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(I) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 33..135

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100

region 1..103 id T11164

est

(ix) FEATURE:

(A) NAME/KEY: other (B) LOCATION: 133..223

(C) IDENTIFICATION METHOD: blastn (D) OTHER INFORMATION: identity 98

region 102..192 id T11164

est

(1x) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 18..140

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.1

seq GILILWIIRLLFS/KT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

AAAGGAAGUG GOTAACT		ACG GAG CAG TGG Thr Glu Gln Trp -35	
GAG ATG STA CAS GC Slu Met Val Sin Al -30			
GAA GGG ATT OTS ATG Glu Gly Ile Leu Ile -1	e Leu Trp Ile Ile		
TAC AAA TTA CAA GA Tyr Lys Leu Gln Gl 5			
CTG ATT GAA GAG TGG Leu Ile Glu Glu Try 20			
GAC CAT CCT GCT CTC Asp His Pro Ala Let 35			
AAA ACT GTG GTG AA Lys Thr Val Val Asi 5	n Gly Lys Glu Cys		
THE OTH SOA THE TR Pho Let Sty Let Let			
TUT CTA AAS AAG TA Ser Led Lys Lys Ty: 85			425

- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Substantia nigra
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 147..328
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 97

region 124..305

id W16517

est

- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 33..149
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 98

region 7..123

id W16517

est

- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 326..385
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 96

region 302..361

id W16517

est

- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 15..149
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 97

region 10..144

id H23328

est

- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 147..276
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 96

region 145..274

id H23328

est

- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 276..309
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 94

region 275..308

id H23328

est

			1R	

- (A) NAME/KEY: other
- (B) LOCATION: 147..309
- (C) IDENTIFICATION METHOD: blastn \cdot
- (D) OTHER INFORMATION: identity 97

region 146..308

id H06320

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 73..149
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 69..145

id H06320

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 5..40
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 1..36

id H06320

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 146..182
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 222..258

id T62763

est

(1x) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 162..398
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1

seq QGVLFICFTCARS/FP

(M1) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

AAAAACTGAJ GOOTGGGASO AGGAACCTGT AGGCAGCGCT TGAGGGTAGG GGGATAGCAG 60

CTGCAACGCG CGTGGGAGGC GGGGGCTCTG GGCGGAACAA AAATCACAGG ATGTCAGAGG 120

ATGTTTCCCG GGAAGAACTG GGATAAAGGG GTCCCAGCAC C ATG GAG GAC CCG AAC 176

Met Glu Asp Pro Asn

-75

מריי שונה הוא השני ביו האו השני הבי חשת השני חשת השני ביו באו האו המה החש ביו השני ביו ביו ביו ביו החשי

Gln Ser Pro Gly Gly Asn Ile Cys His Leu Gly Ala Pro Lys Cys Thr -45

CGC TGC CTC ATC ACC TTC GCA GAT TCC AAG TTS SAG GAG CGT CAC ATG Arg Cys Leu Ile Thr Phe Ala Asp Ser Lys Xaa Xaa Glu Arg His Met -30

AAG CGG GAG CAC CCA GCG GAC TTC GTG GCC CAG AAG CTG CAG GGG GTC ACC ATG Arg Arg Arg Glu His Pro Ala Asp Phe Val Ala Gln Lys Leu Gln Gly Val -25

CTC TTC ATC TGC TTC ACC TGC GCC CGC TCC TTC CCC TCT 407

(2) INFORMATION FOR SEQ ID NO: 257:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 490 base pairs

Leu Phe Ile Cys Phe Thr Cys Ala Arg Ser Phe Pro Ser

- 5

- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(166..452)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 16..302 id AA062591

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 401..445
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100

region 1..45 id AA158358

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 444..490
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93

region 43..89

id AA158358 est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 401..445

540			•	417		
(C)	IDENTIFICATION	METHO	D:	blas	tn	
(D)	OTHER INFORMAT	ION:	1 d e	entit	У	100
			reg	gion	1.	. 45
			id	AA15	84	31
			est	:		
EAT	URE:					

(ix) FEATURE:

- (A) NAME/KEY: other (B) LOCATION: 444..490
- (C) IDENTIFICATION METHOD: blastn(D) OTHER INFORMATION: identity 93

region 43..89 id AA158431

est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 65..160
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1

seq RLLSSLLLTMSNN/NP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

AAGGATCCTC TACC	GGCTTT TCGAGT	CAGT GCTGCCG	SCCG CTGCCCGCGG	CTTTGCAGAG 60								
CAGG ATG AAT GTG ATA GAC CAC GTG CGG GAC ATG GCG GCC GCG GGG CTG 1 Met Asn Val Ile Asp His Val Arg Asp Met Ala Ala Ala Gly Leu -30 -25 -20												
	Arg Leu Leu		TTA CTT ACA ATG Leu Leu Thr Met -5									
			AAG TAC CAG CTT Lys Tyr Gln Leu 10									
			GAA TAT CGG AAT Glu Tyr Arg Asn									
			AAA GCG CTA AGT Lys Ala Leu Ser 45									
			GCA TCT ACT CCA Ala Ser Thr Pro 60									
			TAC AAA ATG GCT Tyr Lys Met Ala 75									
	AAA CAA GAT .		ATT GCT ATA CTT	SAT GGG 445								

TT - 3 - MH - ME -

100

105

110

(2) INFORMATION FOR SEQ ID NO: 258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..337
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 1..312 id HSC26F061

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 97..337
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91

region 20..260

id W30546

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 97..283
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91

region 66..252

id H34739

est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 125..298
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1

seq LVHHCPTWQWATG/EE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

AGGGTGCTGC CWKCCGGGTG CTGWTGCGAG TCGGTGGCAG CGAGGACATT TTCTGACTCC

STGGSSCCTG ACACGGCTGC ACTITICATE CEGTEGEGGG GEEGGEEGET ACTEEGGEEC 120

CAGG ATG CAG AAT GTG ATT AAT ACT GTG AAG GGA AAG GCA CTG GAA GTG 169
Met Gln Asn Val Ile Asn Thr Val Lys Gly Lys Ala Leu Glu Val

-50 -55 -45

GCT GAG TAC CTG ACC CCG GTC CTC AAG GAA TCA AAG TTT AAG GAA ACA 217 Ala Glu Tyr Leu Thr Pro Val Leu Lys Glu Ser Lys Phe Lys Glu Thr -35 GGT GTA ATT ACC CCA GAA GAG TTT GTG GCA GCT GGA GAT CAC CTA GTC 265 Gly Val Ile Thr Pro Glu Glu Phe Val Ala Ala Gly Asp His Leu Val -20 CAC CAC TGT CCA ACA TGG CAA TGG GCT ACA GGG GAA GAA TTG AAA GTG 313 His His Cys Pro Thr Trp Gln Trp Ala Thr Gly Glu Glu Leu Lys Val AAG GCA TAC CTA CCA ACA GGC AAA TGG 340 Lys Ala Tyr Leu Pro Thr Gly Lys Trp

(2) INFORMATION FOR SEQ ID NO: 259:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Colon
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 116..289
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 99

region 89..262

id W68068

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (E) LCCATION: 360..428
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 334..402

id W68068

est

(ix) FEATURE:

- (A) NAME/KEY: other
- BY LOCATION: 286..347
- C IDENTIFICATION METHOD: blastn

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 66..114
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 40..88

id W68068

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..69
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95

region 1..44

id W68068

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 428..465
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 401..438

id W68068

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 66..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 62..285

id AA083574

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 3..45
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 1..43

id AA083574

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 401..444
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93

region 401..444

id AA083574

est

(ix) FERTURE:

- (A) NAME/KEY: other
- (B) LOCATION: 314..347
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 312..345

id AA083574

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) EOCATION: 286..316
- (3) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96

region 283..313 id AA083574

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 127..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 102..264 id AA001460

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 360..465
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 336..441

id AA001460

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 286..347
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 262..323

id AA001460

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (E) LOCATION: 52..103
- (I) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 28..79

id AA001460

est

(1x) FEATURE:

- (%) NAME/KEY: other
- (B) LOCATION: 113..289
- (3) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 78..254

id H72445

est

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region 252..313 id H72445 est

(ix) FEATURE:

(A) NAME/KEY: other(B) LOCATION: 66..113

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100

region 32..79 id H72445

(ix) FEATURE:

(A) NAME/KEY: other(B) LOCATION: 34..69

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 94

region 1..36 id H72445

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 382..411

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 90

region 349..378 id H72445

est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 209..472

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.1

seq CIQRLPWLLLCRG/IT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

AGATCCCGCC TGGGGCCGGC TGAGTGGCAC TTAAGCGGGC CATGCCATGC	60
GCTGCCAACC GTGGGCGAGC TCTGGGTGTG CGGGGGGCCT GGCGCGGCGC	120
CAGCGTGTTA TGATGCCGTC CCGTACCAAC CTGGCTACTG GAATCCCCAG TAGTAAAGTG	180
AAATATTCAA GGCTCTCCAG CACAGACG ATG GCT ACA TTG ACC TTC AGT TTA Met Ala Thr Leu Thr Phe Ser Leu -85	232
AGA AAA CCC CTC CAA AGA TCC CTT ATA AGG CCA TCG CAC TTG CCA CTG Arg Lys Pro Leu Gln Arg Ser Leu Ile Arg Pro Ser His Leu Pro Leu -80 -75 -70 -65	230
TGC TGT TTT GAT TGG CGC CTT TCT CAT TAT TAT AGG CTC CCT CCT GCT Cys Cys Phe Asp Trp Arg Leu Ser His Tyr Tyr Arg Leu Pro Pro Ala -60 -55 -50	328
GTC AGG CTA CAT CAG CAA AGG GGG GGC AGA CCG GGC CGT TCC AGT GCT Val Arg Leu His Gln Gln Arg Gly Gly Arg Pro Gly Arg Ser Ser Ala	376

wo	99/06	548			421									PCT/IB98/01222		
		-45				-40					-35	•				
				GTT Val			-							424		
				AGG Arg -10										472		
 ACT Thr														481		

(2) INFORMATION FOR SEQ ID NO: 260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(V1) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 67..218
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 51..202

id N55991

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (E) LOCATION: 15..74
- (C) IDENTIFICATION METHOD: blastn
- (5) OTHER INFORMATION: identity 100

region 1..59

id N55991

est

: M1 FEATURE:

- (A) NAME/KEY: other
- (F) LOCATION: 89..231
- (0) IDENTIFICATION METHOD: blastn
- (U) OTHER INFORMATION: identity 99 region 1..143

id R57473

est

(D) OTHER INFORMATION: identity 97

region 143..250

id R57473

est

(ix) FEATURE:

- (A) NAME/KEY: other(B) LOCATION: 140..243
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 94

region 195..298

id H79944

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 243..279
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91

region 299..335

id H79944

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 140..237
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92

region 97..194

id H70394

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (E) LOCATION: 235..325
- (C) IDENTIFICATION METHOD: blastn
- (I) OTHER INFORMATION: identity 93

region 193..283

id H70394

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 140..325
- (C) IDENTIFICATION METHOD: blastn
- (0) OTHER INFORMATION: identity 93

region 80..265

id W31972

est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (E) LOCATION: 123..269
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (E) OTHER INFORMATION: score 4

seq PSLAAGLLFGSXA/GL

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

TCC	GCGG	GCC	TTCG	GCAG	AT G	CAGG	CCTG	G GG	TAGT	CTCC	TTT	CTGG	ACT	GAGA	AGAGA	120
				Pro					Val					TTT (Phe (167
										Gly				TAT Tyr -20		215
				Val										GGC Gly		263
							Gln							AAC Asn		311
	Gly		CTA Leu													338

(2) INFORMATION FOR SEQ ID NO: 261:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 302 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 95..241
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 98

region 92..238 id R27748

est

.im FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..90
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97 region 1..89 id R27748

est

(D) OTHER INFORMATION: identity 97

region 116..252

. id T79527

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..47
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 11..56

id T79527

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..90
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 61..98

id T79527

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 95..195
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 59..159

id R08734

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 194..241
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93

region 159..206

id R08734

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (3) LOCATION: 48..90
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 14..56

id R08734

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..298
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92

region 32..228

id H35655

est

im FEATURE:

(A) NAME/KEY: other

- (B) LOCATION: 102..298
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: .identity 90

region 108..304 id AA038389

est

- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: 108..161
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4

seq VAVGLTIAAAGFA/GR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

AGG	GGGT	rsc (GTCG(CTCT	CT GO	GTAAA	AGGC	3 TG	CAGG	rgtt	GGC	CGCG	GCC T	rerga	AGCTG	Ĝ	60
GAT	GAGC(CGT(SCTC	CCGG	rg g/	AAGC <i>i</i>	AAGG(GA(GCCC	CAGC	SGG	AGCC		GCC Ala			116
						CTG Leu											164
						ATG Met											212
						AAA Lys											260
						ATG Met 40											302

(2) INFORMATION FOR SEQ ID NO: 262:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 465 base pairs
 - (P) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR
- :: MOLECULE TYPE: CDNA
- VIL ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
- ik' FRATURE:
 - 'A' NAME/KEl: other

426

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 33..130

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98

region 1..98 id T32007

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 130..314

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98

region 76..260

id R19207

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 53..130

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100

region 1..78 id R19207

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 130..314

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98

region 76..260

id R36562

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 53..130

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100

region 1..78

id R36562

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 130..314

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98

region 76..260

id R59039

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 71..130

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98

region 19..78 id R59039 . est

1	iх) E	ΈĀ	ጥተ	113	F	
- 1	T -1		En		ハヤノ	-	٠

(A) NAME/KEY: other
(B) LOCATION: 130..314

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98

region 70..254

id T35666

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 59..130

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100

region 1..72 id T35666

est

(1x) FEATURE:

(A) NAME/KEY: sig peptide

(B) LOCATION: 136..384

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4

seq AFSFSRLLSQCRP/DC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

AAAGTTCTCC TTCCACCTTC CCCCACCCTT CTCTGCCAAC CGCTGTTTCA GCCCCTAGCT	60
GGATTOCAGO CATTGCTGCA GCTGCTCCAC AGCCCTTTTC AGGACCCAAA CAACCGCAGC	120
CGCTGTTCCC CAGGR ATG GTG ATC CGT GTA TAT ATT GCA TCT TCC TCT GGC Met Val Ile Arg Val Tyr Ile Ala Ser Ser Ser Gly -80 -75	171
TCT ACA GCG ATT AAG AAG AAA CAA CAA GAT GTG CTT GGT TTC CTA GAA Ser Tnr Ala Ile Lys Lys Lys Gln Gln Asp Val Leu Gly Phe Leu Glu -70 -65 -60	219
GCC AAC AAA ATA GGA TTT GAA GAA AAA GAT ATT GCA GCC AAT GAA GAG Ala Asn Lys Ile Gly Phe Glu Glu Lys Asp Ile Ala Ala Asn Glu Glu -55 -45 -40	267
AAT CGG AAG TGG ATG AGA GAA AAT GTA CCT GAA AAT AGT CGA CCA GCG Asn Arg Lys Trp Met Arg Glu Asn Val Pro Glu Asn Ser Arg Pro Ala -35 -30 -25	315
GTT CAS GGG CCA CAT GCT TTT CGG TAT AAA GCA TTC TCC TCC TCT AGG Val Gln Gly Pro His Ala Phe Arg Tyr Lys Ala Phe Ser Phe Ser Arg -20 -15 -10	363
numb out most and mad not come and mad and not come not come not made	

Ser Gln Tyr Cys Leu Tyr Leu Val Met Glu Lys Ala Leu Leu Phe Phe 10 20 25

TTT TTT Phe Phe

465

(2) INFORMATION FOR SEQ ID NO: 263:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 401 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 132..289
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 99

region 117..274

id R14800

est

- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 15..130
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 93

region 1..116

id R14800

est

- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 315..368
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 96

region 302..355

id R14800

est

- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 284..316
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 100

region 270..302

id R14800

est

- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 132..330

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98

region 113..311

id R59757

est

(1x) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 54..130

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93

region 36..112

id R59757

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 18..58

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 92

region 1..41

id R59757

est

(1x) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 132..330

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98

region 94..292

id R25047

est

(1x) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 54..130

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 94

region 17..93

id R25047

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 59..352

(C) IDENTIFICATION METHOD: blastn

(D) GTHER INFORMATION: identity 99

region 38..331

id R23993

est

(im) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 163..294

(C) IDENTIFICATION METHOD: blastn

O) OTHER INFORMATION: identity 92

	 (A) NAME/KEY: other (B) LOCATION: 132194 (C) IDENTIFICATION METHOD: blastn (D) OTHER INFORMATION: identity 90	
(ix)	FEATURE: (A) NAME/KEY: other	
	(B) LOCATION: 305354 (C) IDENTIFICATION METHOD: blastn (D) OTHER INFORMATION: identity 96 region 308357 id W23811 est	
(ix)	FEATURE:	
	(A) NAME/KEY: other (B) LOCATION: 350390	
	(C) IDENTIFICATION METHOD: blastn (D) OTHER INFORMATION: identity 92	
	region 35439; id W23811 est	
(ix)	FEATURE:	
	 (A) NAME/KEY: sig_peptide (B) LOCATION: 243368 (C) IDENTIFICATION METHOD: Von Heijne matrix (D) OTHER INFORMATION: score 4 seq ITSSLFLGRGSVA/SN 	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 263:	
AAGAAGCCGG	TGGCCGCGCA GGAGGACGGA GCCCTAACCG CAACCCGCGC CGCGCCGCGC	60
CGATTTGATT	TGTATCCACT GTCACCAGCA CTGCTCACTT AGGACTTTOT GGATCCAGAC	120
CCAGGCAGCG	CACACTGGAC TCTTGAGGAA GAAGGAGACT CTAATTTTGG ATTCCTTGGT	180
GGAGGAAAAT	AAAACACTCT GGTCTTGCCG CCAACGATGC AAGTGTGACT GCTGGCGTCT	240
Met Ser	TCC AGA GGT CAC AGC ACG CTA CCA AGG ACT CTC ATG GCC Ser Arg Gly His Ser Thr Leu Pro Arg Thr Leu Met Ala -40 -35	287
CCT CGG ATO Pro Arg Met -25	G ATT TOO GAG GGA GAC ATA GGA GGC ATT GOT CAA ATC ACC Tile Ser Glu Gly Asp Ile Gly Gly Ile Ala Gln Ile Thr -20 -15	335
ICC TCT CTA Ser Ser Leu -10	A TIC CTG GGC AGA GGC AGT GTG GCC TCC AAI CGG CAC CTC Phe Leu Gly Arg Gly Ser Val Ala Ser Asn Arg His Leu -5 1 5	333
	C CGT GGC ATC A Arg Gly Ile 10	401

110 33/00348		431		rc	1/1070
(2) INFORMATION	FOR SEQ ID NO: 264:				
(A) (B) (℃)	NCE CHARACTERISTICS: LENGTH: 230 base pa TYPE: NUCLEIC ACID STRANDEDNESS: DOUBL TOPOLOGY: LINEAR	irs			
(ii) MOLEC	CULE TYPE: CDNA				
(A)	NAL SOURCE: ORGANISM: Homo Sapi TISSUE TYPE: Dystro				
(B) (C)	PRE: NAME/KEY: other LOCATION: 47228 IDENTIFICATION METHO OTHER INFORMATION:		183		
(B) (C)	RE: NAME/KEY: other LOCATION: complement IDENTIFICATION METHO OTHER INFORMATION:	DD: blastn	440		
(B) (C)	RE: NAME/KEY: sig_peptic LOCATION: 66119 IDENTIFICATION METHO OTHER INFORMATION:	DD: Von Heij			
(x1) SEQUE	NCE DESCRIPTION: SEC	Q ID NO: 264	1:		
AGGAAGTTCC GGGCC	GAGTT CCTCGTGCCA AC	GTGTCTTG TA	AGGTGCGG CT	AGAAACTG	60
	CG CCT GGC CCA GCG C B Pro Gly Pro Ala L -15				110

ACC CTC ACC GCC CCG CGG CAG AAA ATT ACC AAA GAA ATG GAT GAC TTC 158

206

Inr Leu Thr Ala Pro Arg Gln Lys Ile Thr Lys Glu Met Asp Asp Phe

CTA CAA AAA TTG AGG CAG AAG ATC AAA ATC GGA GTG GTA GGC GGA TCG

Let Glm Lys Let Arg Glm Lys Ile Lys Ile Gly Val Val Gly Gly Ser

(2) INFORMATION FOR SEQ ID NO: 265;

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 224 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 101..220
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 97

region 159..278

id H97758

est

- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 50..103
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 100

region 107..160

id H97758

est

- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 101..185
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 97

region 166..250

id N59486

est

- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 50..103
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 100

region 114..167

id N59486

est

- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 50..103
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 100

region 148..201

id R09724

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 5..54
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100 region 2..51

id R09724 est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 101..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96

region 200..229

id R09724

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 101..178
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 170..247

id W90369

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..103
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 121..171

id **W903**69

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 173..218
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91

region 240..285

id W90369

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (5) LCCATION: 14..103
- [7] IDENTIFICATION METHOD: blastn
- (E) OTHER INFORMATION: identity 100

region 1..90

1d N56221

est

(1x; FEATURE:

'A) NAME/KEY: sig_peptide
'P LOCATION: 126, 182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

ACTGGAAGAA CTCGTCATGC TCTTTGTAGC GTGGTGCTTC TGTTGCTCAC AGGACAACTT 60

GCCTTTGATG ATTTTCAAGA GAGTTGTGCT ATGATGTGGC AAAGTATGCA GGAAGCAGGC 120

GGTCA ATG CCT CTG GGA GCA AGG ATC CTT TTC CAC GGT GTG TTC TAT GCC 170

Met Pro Leu Gly Ala Arg Ile Leu Phe His Gly Val Phe Tyr Ala -15 -10 -5

GGG GGC TTT GCC ATT GTG TAT TAC CTC ATT CAA AAG TTT CAT TCC AGG Gly Gly Phe Ala Ile Val Tyr Tyr Leu Ile Gln Lys Phe His Ser Arg 1 5 10

ACA CTG

(2) INFORMATION FOR SEQ ID NO: 266:

Thr Leu

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 326 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Cancerous prostate
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 24..239
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 99 region 1..216 id HUM429E038 est
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 235..327
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 96 region 211..303 id HUM429E03B est
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 124..327
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 99 region 107..310 id T80259 est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 31..130 .
- (C) IDENTIFICATION METHOD: blastn
- (D) GTHER INFORMATION: identity 95

region 15..114

id T80259 est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 39..283
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95

region 1..245

id T31768

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 271..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 234, 290

id T31768

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96

region 47..272

id N32697

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..97
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 1..43

id N32697

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (E) LOCATION: 65..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96

region 1..263

id N44613

est

thi FEATURE:

(A. NAME/KEY: sig_peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

GCC	TAGG	TGT '	TGTC	GTCC	CT G	CTAG'	TACT	C CG	GGCT	GTGG	GGG	TCGG	TGC	GGAT.	ATTCA	G 60
TCA	TGAA	ATC Z	AGGG'	TAGG	GA C	TTCT	CCCG	C AG	CGAC	GCGG	CTG	GCAA	GAC	TGTT	TGTGT	T 120
GCG	GGGG	CCG (GACT'	rcaa:	GG T	GATT'	TTAC?	A AC				Leu :		ATA (173
ATG Met	CTC Leu	ATG Met -5	CTG Leu	TCA Ser	GCC Ala	ACA Thr	CAA Gln 1	GTC Val	TAC Tyr	ACC Thr	ATC Ile 5	TTG Leu	ACT Thr	GTC Val	CAG Gln	221
CTC Leu 10	TTT Phe	GCA Ala	TTC Phe	TTA Leu	AAC Asn 15	CTA Leu	CTG Leu	CCT Pro	GTA Val	GAA Glu 20	GYA Xaa	GAC Asp	ATT Ile	TTA Leu	GCA Ala 25	269
TAT Tyr	AAC Asn	TTT Phe	GAA Glu	AAT Asn 30	GCA Ala	TCT Ser	CAG Gln	ACA Thr	TTT Phe 35	GAT Asp	GAC Asp	CTC Leu	CCT Pro	GCA Ala 40	AGA Arg	317
	GGT Gly															326

(2) INFORMATION FOR SEQ ID NO: 267:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 398 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Uterus

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 28..395

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96 region 1..368

id AA150637

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 33..297

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99

region 30..294

id H02768

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 181..372
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96

region 148..339

id H70139

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..179
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 1..147

id H70139

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement (267..394)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90

region 231..358

id W46236

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(184..277)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 349..442

id W46236

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (3) LOCATION: complement (109..164)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 464..519

id W46236

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 188..366
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 72..250

id N30922

est

(in FEATURE:

- (A) NAME/KEY: other
- 48) LOCATION: 117..180

- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: 111..185
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 3.9

seq WIAAVTIAAGTAA/IG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

AAT	CGCG	GAG	TCGG	TGCT	TT A	GTAC	GCCG	C TG	GCAC	CTTT	ACT	CTCG	CCG	GCCG	CGCGAA	60
CCC	GTTT	GAG ·	CTCG	GTAT	CC T.	AGTG	CACA	C GC	CTTG	CAAG	CGA	CGGC		ATG . Met . -25		116
CTG Leu	ACT Thr	TCC Ser	AGT Ser -20	TCC Ser	AGC Ser	GTA Val	CGA Arg	GTT Val -15	GAA Glu	TGG Trp	ATC Ile	GCA Ala	GCA Ala -10	GTT Val	ACC Thr	164
ATT Ile	GCT Ala	GCT Ala -5	GGG Gly	ACA Thr	GCT Ala	GCA Ala	ATT Ile 1	GGT Gly	TAT Tyr	CTA Leu	GCT Ala 5	TAC Tyr	AAA Lys	AGA Arg	TTT Phe	212
TAT Tyr 10	GTT Val	AAA Lys	GAT Asp	CAT His	CGA Arg 15	AAT Asn	AAA Lys	GCT Ala	ATG Met	ATA Ile 20	AAC Asn	CTT Leu	CAC His	ATC Ile	CAG Gln 25	260
AAA Lys	GAC Asp	AAC Asn	CCC Pro	AAG Lys 30	ATA Ile	GTA Val	CAT His	GCT Ala	TTT Phe 35	GAC Asp	ATG Met	GAG Glu	GAT Asp	TTS Xaa 40	RNA Xaa	308
GAT Asp	AAA Lys	GCT Ala	GTG Val 45	TAC Tyr	TGC Cys	CGT Arg	TGT Cys	TGG Trp 50	AGG Arg	TCC Ser	AAA Lys	AAG Lys	TTC Phe 55	CCA Pro	TTC Phe	356
TGT Cys	GAT Asp	GGG Gly 60	GCT Ala	CAC His	ACA Thr	ARM Xaa	VAT Xaa 65	AAC Asn	GAA Glu	GAG Glu	ACT Thr	GGG Gly 70	CTG Leu			398

(2) INFORMATION FOR SEQ ID NO: 268:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 393 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Cancerous prostate
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 55..150
 - (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97

region 31..126 .id AA094226

est

(1x) FEATURE:

- (A) NAME/KEY: other
 (B) LOCATION: 151..212
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100

region 126..187

id AA094226

est

(1x) FEATURE:

- (A) NAME/KEY: other
 (B) LOCATION: 24..58
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 1..35 id AA094226

est

(ix) FEATURE:

- (A) NAME/KEY: other
 (B) LOCATION: 211..242
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96

region 185..216 id AA094226

est

(ix) FEATURE:

- (A) NAME/KEY: other
 (B) LOCATION: 55..263
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96

region 202..410

id R54574

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..58
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 172..20%

id R54574

est

ix, FEATURE:

- (A) NAME/KEY: other
- .B: LOCATION: 55..176
- (C) IDENTIFICATION METHOD: blastn
- (D OTHER INFORMATION: identity 98

region 159..280

(B) LOCATION: 174..235

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: . identity 98

region 279..340

id R13710

est

(ix) FEATURE:

- (A) NAME/KEY: other (B) LOCATION: 24..58
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 129..163

id R13710

est

(ix) FEATURE:

- (A) NAME/KEY: other(B) LOCATION: 55..165
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 189..299

id T78111

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 163..203
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92

region 298..338

id T78111

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..58
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 159..193

id T78111

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (E) LOCATION: 201..235
- (C) IDENTIFICATION METHOD: blastn
- (F) OTHER INFORMATION: identity 97

region 337..371

id T78111

est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 70..252
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (0) OTHER INFORMATION: score 3.9

seg YTAVSVLAGPRWA/DP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

AAT	TACG	CAG Z	AGAG.	AAAG'	A TI	CGAG	AAAC'	T CG	TTTT(CATC	TTC	TTGG'	TTT (CATC	YTAAA	т 60
ADDRAAGSTC ATG TOT GGT TOT AAT GGT TOO AAA GAA AAT TOT CAC AAT AAG Met Ser Gly Ser Asn Gly Ser Lys Glu Asn Ser His Asn Lys -60 -55																
	CGG Arg															159
	AAT Asn -30															207
	3AA 31u															255
	CAG Gln															303
	CAT His															351
	AGA Arg 35															393

(2) INFORMATION FOR SEQ ID NO: 269:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 474 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

THE FEATURE:

(A) DAME/KEY: other

(B) LOCATION: 154..352

(C) IDENTIFICATION METHOD: blastn (D) OTHER INFORMATION: identity 93

region 137..335

id HSC1QH021

est

· Frimusu.

region 126..263 id HUML12288 est

(ix) FEATURE:

- (A) NAME/KEY: other(B) LOCATION: 25..111
- (C) IDENTIFICATION METHOD: blastn (D) OTHER INFORMATION: identity 98

region 1..87 id HUML12288

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 178..443
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98 region 1..266 id R60742

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 154..303
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 133..282 id HSC07D011

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..147
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92

region 35..129 id HSC07D011

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..49
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96 region 1..32

id HSC07D011

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 154..298
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 136..280

id C04685

est

(ix) FEATURE:

(A) NAME/KEY: other (B) LOCATION: 25..147

WO 99/06548	443									
	IDENTIFICATION METHOD: blastn OTHER INFORMATION: identity 95 region 10132 id C04685 est									
(3) (C)	CURE: NAME/KEY: sig_peptide LOCATION: 349438 IDENTIFICATION METHOD: Von Heijne matrix OTHER INFORMATION: score 3.9 seq LWMRWTVTSTTRA/WI									
(xi) SEQU	DENCE DESCRIPTION: SEQ ID NO: 269:									
AAAACCTTAG CAAG	SATGGCG GCTCCCTGGG CGTCCCTGCG CCTGGTCGCC CCCATGTGGA	60								
ATGGGCGTAT CAGG	GGGCATC CATCGCCTGG GTGCGGCAGT GGCCCCAGAG GGCAATCAGA	120								
AGAAGAAAAG GACA	NATAMTE CARKTYCETG GMCCVAASTA TTTCTACGAT GTGGAGGETE	180								
TGAGGGATTA CTTG	SCTCCAA AGGGAGATGT ACAAGGTGCA TGAGAAAAAT CGATCTTACA	240								
CCTGGCTGGA GAAG	SCAACAT GGTCCATACG GCGCAGGTGC CTTTTTCATC CTGAAGCAGG	300								
SAGGCGCAGT CAAG	STTTCGA GACAAGGAGT GGATCAGGCC AGATAAGT ATG GCC ATT Met Ala Ile -30	357								
TCT CTC AGG AGT Ser Leu Arg Ser -25	TCT GGA ATT TCT GTG AAG TGC CTG TCG AAG CTG TGG Ser Gly Ile Ser Val Lys Cys Leu Ser Lys Leu Trp -20 -15	405								
ATG CG3 TGG ACT Met Arg Trp Thr -10	GTG ACA TCA ACT ACG AGG GCC TGG ATM RNN GCN GAA Val Thr Ser Thr Thr Arg Ala Trp Ile Maa Ala Glu -5	453								
CCT CCG CAG CTG Pro Pro Gln Leu		474								
'i-seque A:	FOR SEQ ID NO: 270: NGE CHARACTERISTICS: IENGTH: 211 base pairs TYPE: NUCLEIC ACID									
	STRANDEDNESS: DOUBLE									

(2) INFORMA

(D' TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(V1 ORIGINAL SOURCE:

(A) GRGANISM: Homo Sapiens

PCT/IB98/01222

			(C) (D)	IDE OTH	NTIF ER I	ICAT NFOR	ION MATI	METH ON:	ide .reg	ntit ion AA08	tn y 96 49 2886	177				
	(ix)	(A) (B) (C)	NAM LOC	ATIO NTIF	N: 4 ICAT	78 ION	3 METH	ide reg	ntit	y 97 15	51				
<pre>(ix) FEATURE: (A) NAME/KEY: sig_peptide</pre>																
			(B)	LOCATION: 1797												
<pre>(C) IDENTIFICATION METHOD: Von Heijne matrix (D) OTHER INFORMATION: score 3.8</pre>																
	(:	xi) :	SEQU:	ENCE	DES	CRIP	rion	: SE	QID	NO:	270	:				
AAC	ATTA	ACC (GGCA	GG A'	IG TO	er G	AG G' lu Va 25	TG Co	GG C' rg L	TG Co	ro Pa	CG C' ro Le 20	TA Co eu A	GC GG rg Al	CC CTG la Leu	5 52
GAC Asp -15	GAC Asp	TTT Phe	GTT Val	CTG Leu	GGG Gly -10	TCG Ser	GCG Ala	CGT Arg	CTT Leu	GGC Gly -5	GGC Gly	TCC Ser	GGA Gly	TCC Ser	ATG Met 1	100
CGA Arg	CCC Pro	GCT Ala	GCG Ala 5	ATG Met	GTG Val	YHA Xaa	CCG Pro	CGT Arg 10	CAT His	CAA Gln	CAA Gln	CCT Pro	CCT Pro 15	CTA Leu	CTA Leu	148
CCA Pro	AAC Asn	CAA Gln 20	CTA Leu	CCT Pro	TCT Ser	CTG Leu	CTT Leu 25	CGG Arg	CAT His	CGG Arg	CCT Pro	CGC Arg 30	TCT Ser	CGC Arg	CGG Arg	196
		ACG Thr														211
(2)	INFO	ORMAI	ROII	FOR	SEQ	ID N	10: 2	271:								
(B) (C)				LENG TYPE	TH: : NU .NDED	262 CLEI NESS	base C AC : DC	e pai ID UBLE								

(ii) MOLECULE TYPE: CDNA

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Muscle

(vi) ORIGINAL SOURCE:

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 184..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 177..257 id W93162

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 113..183
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95

region 107..177

id W93162

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 184..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 174..254

id W67415

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 62..112
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94

region 52..102

id W67415

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 141..183
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 132..174

id W67415

est

TIK FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 184..264
- AC: IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 174..254

id N44655

est

.

LE FEATURE:

(A) NAME/KEY: other

מסי פני אמדקקממי יפס

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 54..183

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97

region 41..170 id HSBA7H051

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 184..240

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96

region 170..226 id HSBA7H051

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 14..52

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100

region 2.,40 id HSBA7H051

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 77..183

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97

region 63..169

id R37538

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 184..264

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96

region 169..249

id R37538

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 15..53

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100

region 1..39 id R37538

est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 206..250

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.8

seq LVSATAWLEECWW/SE

(xi) SEQUENCE DESCRIPTION: SEQ. ID NO: 271:

ASSOCICA GATGCCGAG AACACCGTC GCCCCGCAA GAGCAGCGGG AGCGNCGCGN 60 GGAASGSGSC GSTGTCCGCA GAGCAGGTGA TTGCTGGCTT CAACCGCCTT CGGCAGGAAC 120 AGGGAGGCT GGCATCCAAA GCAGCTGAGT TGGAGATGGA GTTGAATGAG CACAGCCTAG 180 TGAATOGATA CACTGAAGGA GGTAG ATG AAA CTC GTA AGT GCT ACC GCA TGG 232 Met Lys Leu Val Ser Ala Thr Ala Trp -15 -10TTG GAG GAR TGC TGG TGG AGC GAA CTG TCA 262 Leu Glu Glu Cys Trp Trp Ser Glu Leu Ser

(2) INFORMATION FOR SEQ ID NO: 272:

- 5

(i: SEQUENCE CHARACTERISTICS:

(A) LENGTH: 422 base pairs

B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(i1) MOLECULE TYPE: CDNA

(V1) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 142..382

(C) IDENTIFICATION METHOD: blastr

(D) OTHER INFORMATION: identity 99 region 120..360

id HUML1108

est

(1x) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 29..139

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97

region 17..127

id HUML1108

est

Fix: FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 30..395

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 32..395

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93

region 137..500 id HSU51712

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 237..395

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100

region 112..270

id T70871

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 133..235

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98

region 9..111 id T70871

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 77..185

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96

region 105..213

id H48308

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 177..286

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 95

region 206..315

id H48308

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 284..317

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 94

region 314..347

id H48308

est

(ix) FEATURE:

(A) NAME/KEY: sig peptide

(B) LOCATION: 309..410

(C) IDENTIFICATION METHOD: You Heijne matrix

(D) OTHER INFORMATION: score 3.3

seq LYVPLLAVCCLHS/WW

(N1) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

AAGCTTCCAA ACCCAGGGCT TGCGCTTGCC TTTGCCTCTT CCACCGCGCA GGGACCATGT	60
CGGCGGAGAC CGCGAGAGGG ACCAGGTGGA AATCCTGGAG TACAACTTCA	120
ACAAGGTEGA CAAGCACCCG GATTCCACCA CGCTGTGCCT CATCGCGGCC GAGGCAGGCC	180
TTTCCGAGGA GGAGACCCAG AAATGGTTTA AGCAGCGCCT GGCAAAGTGG CGGCGCTCAG	240
AAGGCCTGCC CTCAGAGTGC AGATCCGTCA CAGACTAAGG AGATGGCAGG CATTGACAGC	300
TTCASTCC ATG AAG GCC ATC TCT GTT TCT CTC CTC CGC TTA ACC AAG CTG Met Lys Ala Ile Ser Val Ser Leu Leu Arg Leu Thr Lys Leu -30 -25	350
TTG TGG TTT TTC AGC ATA GTG TTG TAT GTT CCA TTG CTA GCT GTC TGC Leu Trp Phe Phe Ser Ile Val Leu Tyr Val Pro Leu Leu Ala Val Cys -20 -15 -5	398
TGT TTA CAC AGT GTT GTA TTT TTT Cys Leu His Ser Val Val Phe Phe	422

(2) INFORMATION FOR SEQ ID NO: 273:

(1' SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(VI) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Thyroid

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 195..421
- (C) IDENTIFICATION METHOD: plastn
- 'D' OTHER INFORMATION: identity 96 region 179..400 10 AA010986 est

Gim' FEATURE:

- (A) NAME/KEY: other
- B. LOCATION: 20..109
 TO IPENCIFICATION METHOD: blastn
- TO OTHER INFORMATION: Identity 130

- (A) NAME/KEY: other(B) LOCATION: 108..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93 region 91..188 id AA010986

est

(ix) FEATURE:

- (A) NAME/KEY: other
 (B) LOCATION: 443..505
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95

region 429..491 id AA010986

est

(ix) FEATURE:

- (A) NAME/KEY: other(B) LOCATION: 417..449
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90

region 402..434 id AA010986

est

(ix) FEATURE:

- (A) NAME/KEY: other
 (B) LOCATION: 19..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95

region 1..187 id W96112

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 316..494
- (C) IDENTIFICATION METHOD: blastn (D) OTHER INFORMATION: identity 92

region 300..478

id W96112

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 195..336
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95

region 178..319

id W96112

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 69..513
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 1..445

id W44481

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 14..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96

region 2..193 id AA129812

est

(ix) FEATURE:

- (A) NAME/KEY: other (B) LOCATION: 195..300
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 184..289 id AA129812

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 349..405
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92

region 340..396

id AA129812

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (E) LOCATION: 301..352
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92

region 291..342

id AA129812

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 405..448
- (C) IDENTIFICATION METHOD: blastn
- (D) GTHER INFORMATION: identity 97

region 397..440

1d AA129812

est

(1x1 FEATURE:

- (A) NAME/KEY: other
- (L) LOCATION: 2..290
- (C) IDENTIFICATION METHOD: blastn
- (I) OTHER INFORMATION: identity 97

region 1..200

id W40172

est

IN FEATURE:

id W40172 est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 285..342

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93

region 285..342

id W40172

est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 85..438

(C) IDENTIFICATION METHOD: Von Heijne matrix

ACTCCAACGC TGGGTGACAT TGAGCTCACC AGCGCCACCG TCCCCGGCGA AGTTCTGCGC 60

(D) OTHER INFORMATION: score 3.8

seq LMIALTVVGCIFM/VI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

	0.0
TGGTCGGCGG AGTAGCAAGT GGCC ATG GGG AGC CTC AGC GGT CTG CGC CTG Met Gly Ser Leu Ser Gly Leu Arg Leu -115 -110	111
GCA GCA GGA AGC TGT TTT AGG TTA TGT GAA AGA GAT GTT TCC TGN TCT Ala Ala Gly Ser Cys Phe Arg Leu Cys Glu Arg Asp Val Ser Xaa Ser -105 -100 -95	159
CTA AGG CTT ACC AGA AGC TCT GAT TTA AAG AGA ATA AAT GGA TTT TGC Leu Arg Leu Thr Arg Ser Ser Asp Leu Lys Arg Ile Asn Gly Phe Cys -90 -85	207
ACA AAA CCA CAG GAA AGT CCC GGA GCT CCA TCC CGC ACT TAC AAC AGA Thr Lys Pro Gln Glu Ser Pro Gly Ala Pro Ser Arg Thr Tyr Asn Arg -75 -70 -68	255
GTG CCT TTA CAC AAA CCT ACG GAT TGG CAG AAA AAG ATC GTG ATA TGG Val Pro Leu His Lys Pro Thr Asp Trp Gln Lys Lys Ile Leu Ile Trp -60 -55 -50	303
TCA GGT CGC TTC AAA AAG GAA ANB NAA ATC CCA GAG ACT STC TCG TTG Ser Gly Arg Phe Lys Lys Glu Xaa Xaa Ile Pro Glu Thr Val Ser Leu -45 -35 -30	351
GAG ATG CTT GAN STT GCA AAG AAC AAG ATG CGA GTG AAG ATC AGC TAT Glu Met Leu Xaa Xaa Ala Lys Asn Lys Met Arg Val Lys Ile Ser Tyr -25 -20 -15	399
CTA ATG ATT GCC CTG ACG GTG GTA GGA TGC ATC TTC ATG GTT ATT GAG Leu Met Ile Ala Leu Thr Val Val Gly Cys Ile Phe Met Val Ile Glu -10	447
GGC AAG AAG GCT GCC CAA AGA CAC GAG ACT TTA ACA AGC TTG MAC TTA Gly Lys Lys Ala Ala Gln Arg His Glu Thr Leu Thr Ser Leu Xaa Leu 5 10	495
GAA AAG AAA GCT CGT CTG	513

```
Glu Lys Lys Ala Arg Leu
20
```

(2) INFORMATION FOR SEQ ID NO: 274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(1x) FEATURE:

- (A) NAME/KEY: other
- (5) LOCATION: 198..407
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 190..399 id AA001815

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 41..147
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 35..141

1d AA001815

est

(ix) FERTURE:

- (A) NAME/KEY: other
- (B) LOCATION: 146..205
- (C) IDENTIFICATION METHOD: blastn
- (E) OTHER INFORMATION: identity 91

region 139..198

id AA001815

est

1M% FEATURE:

- FA MAME/KEY: other
- /F% 10CATION: 198..400
- (0) IDENTIFICATION METHOD: blastn
- (D OTHER INFORMATION: identity 98

region 139..31;

id N42162

est

IN FEATURE:

```
id N42162
est
```

(ix) FEATURE:

- (A) NAME/KEY: other
 (B) LOCATION: 198..354
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98

region 144..300 id N24414

est

(ix) FEATURE:

- (A) NAME/KEY: other(B) LOCATION: 62..147
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 10..95 id N24414

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 146..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93

region 93..152

id N24414

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 198..414
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 122..339

id W76137

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 75..147
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 1..73

id W76137

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 146..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93

region 71..130

id W76137

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 198..360
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96 region 121..283 id H03817 est (ix) FEATURE: (A) NAME/KEY: other (B) LOCATION: 77..147 (C) IDENTIFICATION METHOD: blastn (D) OTHER INFORMATION: identity 98 region 2..72 id H03817 est (ix) FEATURE: (A) NAME/KEY: other (B) LOCATION: 346..402 (C) IDENTIFICATION METHOD: blastn (D) OTHER INFORMATION: identity 94 region 270..326 id H03817 est (ix) FEATURE: (A) NAME/KEY: other (B) LOCATION: 146..205 (C) IDENTIFICATION METHOD: blastn (D) OTHER INFORMATION: identity 91 region 70..129 id H03817 (ix) FEATURE: (A) NAME/KEY: sig peptide (B) LOCATION: 59..358 (C) IDENTIFICATION METHOD: Von Heijne matrix (D) OTHER INFORMATION: score 3.7 seq LASSFLFTMGGLG/FI (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274: ACTGTTTNNG GGAGGCGCGT GGGGCTTGAG GCCGAGAACG GCCCTTGCTG CCACCAAC 58 ATG GAG ACT TTG TAG CGT GTC CCG TTC TTA GTG CTC GAA TGT CCC AAC 106 Mot Glu Thr Leu Tyr Arg Val Pro Phe Leu Val Leu Glu Cys Pro Asn -100 - 95 -90 TTG AAG CTG AAG AAG CCG CCC TGG TTG CAC ATG CCG TCC GCC ATG ACT 154 Leu Lys Leu Lys Lys Pro Pro Trp Leu His Met Pro Ser Ala Met Thr -80 GTG TAT GCT CTG GTG GTG GTG TCT TAC TTC CTC ATT ACC GGA GGA ATA 202 Val Tyr Ala Leu Val Val Val Ser Tyr Phe Leu Tie Thr Gly Gly Ile -65 -60 -55 The test are some some commisses are some some

- (A) LENGTH: 243 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Cancerous prostate
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 136..238
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 90 region 80..132

id C05215

est

- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: 73..111
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 3.7

seq MLVLPSGLTKALA/SR

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

CACTOGGGAA GACTTCAGAG AAGTSTCACA AAGGACTCGG CIGGGTGCTT TTCTCAGTGC 60

CGAAGCCGCG CC ATG CTC GTT CTC AGA AGC GGC CT3 ACC AAG GCG CTT GCC 111

Met Leu Val Leu Arg Ser Gly Leu Tor Lys Ala Leu Ala
-10 -3

TCA CGG ACG CTC GCG CVT CAG AKA AWT TTT GCT TWT CGA GCT GAA GTT 159

Ser Arg Thr Leu Ala Xaa Gln Xaa Xaa Phe Ala dic Arg Ala Glu Val

1 5 10 15

CGG AAA GCC TTA GCC AAC TGT AAG GAA TGG CAA GAA CAA TCT ATC ATT 207

Arg Lys Ala Leu Ala Asn Cys Lys Glu Trp Gln Glu Gln Ser Ile Ile 20 25 30

CCA AAT TTG GCT CGC ATT GAT AAA CAA GAG ACC AGG Pro Asn Leu Ala Arg Ile Asp Lys Gln Glu Thr Arg

243

(2) INFORMATION FOR SEQ ID NO: 276:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 245 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR
- (11) MOLECULE TYPE: CDNA
- (V1) OFIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Thyroid
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 112..241
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 98

region 77..206

id R87832

est

- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (E) LOCATION: 37..113
 - (C) IDENTIFICATION METHOD: blastn
 - (I) OTHER INFORMATION: identity 92

region 1..77

id R87832

est

- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 112..241
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 98

region 55...194

1d HUM4279109

est

- .ix FEATURE:
 - (A) NAME/KEY: other
 - (B. LOCATION: 49..113
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 94

region 1...

-	
06548	458
(C)	LOCATION: 112241 IDENTIFICATION METHOD: blastn OTHER INFORMATION: identity 98 region 52181 id R52722 est
FEAT	URE:
(B) (C)	NAME/KEY: other LOCATION: 62113 IDENTIFICATION METHOD: blastn OTHER INFORMATION: identity 92 region 152 id R52722 est
FEAT	URE:
(B) (C)	NAME/KEY: other LOCATION: 111241 IDENTIFICATION METHOD: blastn OTHER INFORMATION: identity 90 region 79209 id W41484 est
FEAT	
(B) (C)	NAME/KEY: sig_peptide LOCATION: 30137 IDENTIFICATION METHOD: Von Heijne matrix OTHER INFORMATION: score 3.7 seq NIESLAWTGGTLG/HP

(ix)

(ix)

(ix)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

GAGTTTCCTG C	CGAGCTCGGC TTCCTCAAC		G CCC TTG TCA a Pro Leu Sei		3
GTG GAG TTC Val Glu Phe	GGA GGT GGT GCG GAS Gly Gly Gly Ala Xaa -25	TCC TGT TTC Ser Cys Lec -20	G ACG GTA TTA u Thr Val Leu -15	a Arg Asn	
	CTT GCC TGG ACA GGA Leu Ala Trp Thr Gly -5	Gly Thr Let)
GCT CAT CTG Ala His Leu 5	GAT CAA GAA GAA TTT Asp Gln Glu Glu Phe 10	GCT AAA AGA Ala Lys Are	g Ala Ala Xaa	GTT GTT 197 Val Val 20	,
	AGA CAG CGT GCG GCC Arg Gln Arg Ala Ala 25				,

(2) INFORMATION FOR SEQ ID NO: 277:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 401 base pairs

- (B) TYPE: NUCLEIC ACID (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (v1) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Umbilical cord
- (ix) FEATURE:
 - (A) NAME/KEY: other (B) LOCATION: 22..403
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 98

region 1..382 id AA127626

est

- (1X) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 64..349
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 98

region 44..329

id W39584

est

- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 349..403
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 96

region 330..384

id W39584

est

- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 24..60
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 100

region 3..39 id W39584

est

- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (F) LCCATION: complement (47..403)
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 93

region 63..424

id N32838

es:

- ik: FEATURE:
 - ্ত্রত স্মুদ্র সেল্প ওচ্চতত দ

id AA121528 est

(ix) FEATURE	Ξ:
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(A) NAME/KEY: other

(B) LOCATION: 164..378

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98

region 130..344 id AA082078

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 36..165

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99

region 1..130 id AA082078

est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 198..392

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.7

seq FVGGLPVIFWSWA/GL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

ACTTAGTCGT GTGTACATCA TTGGGAATGG AGGGAAATAA ATGACTGGAT GGTCGCTGCT	60
TTTTAAGTTT CAAATTGACA TTCCAGACAA GCGGTGCCTG AGCCTGTGCC TGTCTTCAGA	120
TCTTCACAGO ACAGTTCCTG GGAAGGTGGA GCCACCAGCC TCTCCTTGAA TAACTGGGAG	180
ATGAAACAGG AAGCTCT ATG ACA CAC TTG ATC GAA TAT GAC AGA CAC CGA Met Thr His Leu Ile Glu Tyr Asp Arg His Arg -65 -60 -55	230
AAA TCA CGA CTC AGC CCC CTC CAG CAC CTC TAC CTG TTG CCC GCC GAT Lys Ser Arg Leu Ser Pro Leu Gln His Leu Tyr Leu Leu Pro Ala Asp -50 -40	278
CAC AGC CGG AAT GCA GCT GAA AGA TTC CCT GGG GCC TGG TTC CAA CCG His Ser Arg Asn Ala Ala Glu Arg Phe Pro Gly Ala Trp Phe Gln Pro -35 -25	326
CCC ACT GTG GAC TCT GAG GCC TCT GCA TTT GTG GGT GGT CTG CCT GTG Pro Thr Val Asp Ser Glu Ala Ser Ala Phe Val Gly Gly Leu Pro Val -20 -15 -10	374
ATA TIT TGG TCA TGG GCT GGT CTG GTC Ile Phe Trp Ser Trp Ala Gly Leu Val -5 1	401

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(v1) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Uterus

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 70..337
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 1..268 id HSC2SG081

461

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 71..251
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 1..181 id R13964

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 256..334
- (C) IDENTIFICATION METHOD: blastn
- (C) OTHER INFORMATION: identity 100

region 184..262

id R13964

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..255
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94

region 1..230 id HUML13589

est

ik FEATURE:

- (A) NAME/KEY: other
- (8) LOCATION: 116..251
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96

region 1..136

id H05572

est

	W	99 /0	6548						4	62						PCT/IB9
			(D)	OTH	ER I	NFOR	MATI	ON:	reg	ntit ion H055	139.					
	(ix)	(B)	NAM!	ATION NTIF	N: 2 ICAT	48 ION 1	9 METHO	DD:	Von 1 re 3 WAR1	. 7					
	(:	κi) :	SEQUI	ENCE	DES	CRIP'	TION	: SE	QID	NO:	278	:				
AAC	AGTT	ACG (CGCC	GCAC	GG A	TC A	TG G et A	la A	CA G la A 20	CC G	CT C	TG G eu G	ly G	AG A' ln I 15	TC TG0 le Tr	G 53
GCA Ala	CGA Arg	AAG Lys -10	CTT Leu	CTC Leu	TCT Ser	GTC Val	CCT Pro -5	TGG Trp	CTT Leu	CTG Leu	TGT Cys	GGT Gly 1	CCC Pro	AGA Arg	AGA Arg	101
TAT Tyr 5	GCC Ala	TCC Ser	TCC Ser	AGT Ser	TTC Phe 10	AAG Lys	GCT Ala	GCA Ala	GAC Asp	CTG Leu 15	CAG Gln	CTG Leu	GAA Glu	ATG Met	ACA Thr 20	149
CAG Gln	AAG Lys	CCT Pro	CAT His	AAG Lys 25	AAG Lys	CCT Pro	GGC Gly	CCC Pro	GGC Gly 30	GAG Glu	CCC Pro	CTG Leu	GTG Val	TTT Phe 35	GGG Gly	197
AAG Lys	ACA Thr	TTT Phe	ACC Thr 40	GAC Asp	CAC His	ATG Met	CTG Leu	ATG Met 45	GTG Val	GAA Glu	TGG Trp	AAT Asn	GAC Asp 50	AAG Lys	GGC Gly	245
TGG Trp	GGC Gly	CAG Gln 55	CCC Pro	CGA Arg	Ile	Gln	Pro	Phe	Gln	AAC Asn	Leu	Thr	Leu	CAC His	CCA Pro	293

335

(2) INFORMATION FOR SEQ ID NO: 279:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 344 base pairs

GCC TCC TCC AGC CTC CAC TAC TCC CTG CAG CTG TTT GAG GGC

Ala Ser Ser Ser Leu His Tyr Ser Leu Gln Leu Phe Glu Gly 75

- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Hypertrophic prostate
- (ix) FEATURE:
 - (A) NAME/KEY: other

- (B) LOCATION: 57..176
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 50..169 id AA126817

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 219..344
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94

region 213..338

id AA126817

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 10..344
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96

region 2..336

id W79731

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..344
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 1..326

id H21245

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 31..302
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96

region 34..305

id H11314

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 302..344
- (C) IDENTIFICATION METHOD: blastn
- .0) CTHER INFORMATION: identity 97

region 306..348

id H11314

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 41..202
- D IDENTIFICATION METHOD: blastn 12 may 1 may

(ix) FEATURE:

(A) NAME/KEY: other (B) LOCATION: 201..284

(C) IDENTIFICATION METHOD: blastn (D) OTHER INFORMATION: identity 98

region 183..266

id W19587

est

(ix) FEATURE:

(A) NAME/KEY: other(B) LOCATION: 283..344

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96

region 266..327

id W19587

est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 48..161

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.7

seq CPLLLLVFTTNNG/RH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

AAGGGGTCGG AC	GGTCAGGGC GAGG	CGTCTCG CAGGCCGT?		TG GCG GTG et Ala Val	
GAG TCG CGC G Glu Ser Arg V -35	GTT ACC CAG GA Val Thr Gln G1 -30	AG GAA ATT AAG AA lu Glu Ile Lys Ly -2	ys Glu Pro G	AG AAA CCG lu Lys Pro -20	
		GC CCA CTG TTG CT ys Pro Leu Leu Le -10			
AAT AAC GGC C Asn Asn Gly A	CGC CAC CAC CC Arg His His Ar 1	GA ATG GAC GAG TI rg Met Asp Glu Ph 5	TC TCC CGG G ne Ser Arg G 10	GA AAT GTA ly Asn Val	200
CCG TCC AGC G Pro Ser Ser G 15	Glu Leu Gln Il	TC TAC ACT TGG AT le Tyr Thr Trp Me 20	TG GAT GCA AGET ASP Ala TE	CT TTG AAA nr Leu Lys	248
GAA CTG ACA A Glu Leu Thr S 30	AGC TTA GTA AF Ser Leu Val Ly 35	AA GAA GTC TAC CC ys Glu Val Tyr Pr 4	CA GAA GCT A co Glu Ala A 10	GA WAG AAG cg Xaa Lys 45	296
GGC ACT CAC T Gly Thr His F	TTC AAT TTT GC Phe Asn Phe Al 50	DA VTC GTT TTT AC la Xaa Val Phe Th 55	DA GAT GTT A	AA AGA CCT ys Arg Pro 60	344

(2) INFORMATION FOR SEQ ID NO: 280:

(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 401 base pairs

- (B) TYPE: NUCLEIC ACID(C) STRANDEDNESS: DOUBLE(D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 111..377
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 99

region 72..338

id W79829

est

- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 370..401
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 90

region 332..363

id W79829

est

- (1x) FEATUPE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 111..377
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 99

region 14..280

id H62624

est

- (1x) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 370..401
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 90

region 274..305

id H62624

est.

- (1M) FEATURE:
 - (A: NAME/KEY: other
 - (B) 100ATION: 111..3"7
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 99

region 24..290

id H81957

est

region	59.	.324
id W829	998	
est.		

4	ix	FEATURE:	
1	1 X	L LAIUKL:	

- (A) NAME/KEY: other
- (B) LOCATION: 111..376
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92

region 64..329 id AA023811

est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 240..305
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7

seq AVLDCAFYDPTHA/WS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

ACTAGCCTGC GAGTGTTCTG AGGGAAGCAA GGAGGCGGCG GCGGCCGCAG CGAGTGGCGA	60
GTAGTGGAAA CGTTGCTTCT GAGGGGTGTC CAAGATGASC GGTTCKAMCG GAGKTCAAGC	120
TGAACCAGCC ACCCGAGGAT GGCATCTCCT CCGTGAAGTT CAGCCCCAAC ACCTCCCAGT	180
TCCTGCTTGT CTCCTCCTGG GACACGTCCG TGCGTCTCTA CGATGTGCCG GCCAACTCC	239
ATG CGG CTC AAG TAC CAG CAC ACC GGC GCC GTC CTG GAC TGC GCC TTC Met Arg Leu Lys Tyr Gln His Thr Gly Ala Val Leu Asp Cys Ala Phe -20 -15	287
TAC GAT CCA ACG CAT GCC TGG AGT GGA GGA CTA GAT CAT CAA TTG AAA Tyr Asp Pro Thr His Ala Trp Ser Gly Gly Leu Asp His Gln Leu Lys -5 1 5 10	335
ATG CAT GAT TTG AAC ACT GAT CAA GAA AAT CTT GTT GGG ACC ATG ATG Met His Asp Leu Asn Thr Asp Gln Glu Asn Leu Val Gly Thr Met Met 15 20 25	383
CCC CTA TCA GAT GTG TTG Pro Leu Ser Asp Val Leu 30	401

(2) INFORMATION FOR SEQ ID NO: 281:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 275 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Uterus

(ix) FEATURE:

- (A) NAME/KEY: other(B) LOCATION: 87..272
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 72..257 id T60345

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 47..89
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 33..75 id T60345

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 14..47
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97 region 1..34 at T60345

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 87..272
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96 region 75..260 id T46853

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 12..89
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 1..78 id T46853

est

(ix) FRATURE:

- A' NAME/KEY: other
- .B) LOCATION: 87..207
- IDENTIFICATION METHOD: blastn
- DI OTHER INFORMATION: identity 97

region 39..159

id R57601

est

Marie Commence Commen

50

region 144..223 id R57601 est

(ix) FEATURE:

(A) NAME/KEY: other(B) LOCATION: 48..89

(C) IDENTIFICATION METHOD: blastn (D) OTHER INFORMATION: identity 92

region 1..42
id R57601
est

(ix) FEATURE:

(A) NAME/KEY: other(B) LOCATION: 84..195

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 90 region 55..166 id W71083

est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 12..269

(C) IDENTIFICATION METHOD: Von Heijne matrix

ATAGGCGCAA G ATG GCG CTG CTT TTT GCA CGT TCT TTG CGC TTG TGC CGC

(D) OTHER INFORMATION: score 3.7

seq WAVVLADTAVTSG/RG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

Met Ala Leu Leu Phe Ala Arg Ser Leu Arg Leu Cys Arg -85 -80 -75													
	GGA Gly												98
	AGT Ser												146
	AGA Arg -40												194
	AAG Lys												242
	GCA Ala												275

(2) INFORMATION FOR SEQ ID NO: 232:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	397	bas	se :	pairs
(B)	TYPE: NO	JCLEI	C F	CI	D
(3)	STRANDE	DNESS	: E	OU	BLE.

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 77..280

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.6

seq ILLGNYCVAVADA/KK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

ATTCCCCCTT GGGCGGTGGT GGAGGTGGTA ACCGTGATAG TAGCAGCTCC GGCGGCAGCA ACAGOGACTA CGAGGG ATG GCG GCG GCT GCA GCA GCA ACT SNA ACA TCC CAG Met Ala Ala Ala Ala Gly Thr Xaa Thr Ser Gln AGG TIT TIC CAG AGC TIC TCG GAT GCC CTA ATC GAC GAG GAC CCC CAG 160 Arg Phe Phe Gln Ser Phe Ser Asp Ala Leu Ile Asp Glu Asp Pro Gln -55 -50 GOG GOG TTA GAG GAG CTG ACT AAG GCT TTG GAA CAG AAA CCA GAT GAT 208 Ala Ala Leu Glu Glu Leu Thr Lys Ala Leu Glu Gln Lys Pro Asp Asp -35 -30 GCA CAG TAT TAT TGT CAA AGA GCT TAT TGT CAC ATT CTT CTT GGG AAT 256 Ala Gln Tyr Tyr Cys Gln Arg Ala Tyr Cys His Ile Leu Leu Gly Asn -20 TAC TGT GTT GTT GCT GAT GCA AAG AAG TCT CTA GAA CTC AAT CCA 304 Tyr Cys Val Ala Val Ala Asp Ala Lys Lys Ser Leu Glu Leu Asn Pro - 5 AAT AAT TOO ACT GOT ATG CTG AGA AAA GGA ATA TGT GAA TAC CAT GAA 352 Asn Asn Ser Thr Ala Met Leu Arg Lys Gly Ile Cys Glu Tyr His Glu ANA AND THE GOT GOT GOT CHA GAN ACT TIT THE AGA AGG ACG GGG 397

AND INFORMATION FOR SEQ ID NO: 283:

JEQUENCE CHARACTERIUTICS:

30

. to Aprilly this Ala Ala Ala Lyu Glu Tor Phe Tyr Arg Arg Thr Gly

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 78..379
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 79..380

id H17763

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..53
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 4..55

id H17763

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 96..377
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 82..363

id H16532

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..53
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 7..58

id H16532

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 79..370
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 46..337

id R52491

est

(iz: FEATURE:

- (A) NAME/KEY: otner
- (3) LOCATION: 66..248
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96

region 65..247

id R21494

est

471 (ix) FEATURE: (A) NAME/KEY: other (B) LOCATION: 2..53 (C) IDENTIFICATION METHOD: blastn (D) OTHER INFORMATION: identity 100 region 1..52 1d R21494 est (ix) FEATURE: (A) NAME/KEY: other (B) LOCATION: 266..305 (C) IDENTIFICATION METHOD: blastn (D) OTHER INFORMATION: identity 97 region 268..307 id R21494 est (1x) FEATURE: (A) NAME/KEY: other (B) LOCATION: 129...321 (C) IDENTIFICATION METHOD: blastn (D) OTHER INFORMATION: identity 99 region 71..263 id AA084554 est (1x) FEATURE: (A) NAME/KEY: other (B) LOCATION: 315..379 (C) IDENTIFICATION METHOD: blastn (D) OTHER INFORMATION: identity 96 region 256..320 id AA084554 (ix) FEATURE: (A) NAME/KEY: sig_peptide (B) LOCATION: 139..318 (3) IDENTIFICATION METHOD: Von Heijne matrix (D) OTHER INFORMATION: score 3.5 seq WFYIGSSLNGTRG/KR (Ma) SEQUENCE DESCRIPTION: SEQ ID NO: 283: ASTRUCTURE ATOTTOGGTS CARTUTOCCAG ATCCGCTGAT CTAGTGCTTC TCGAAAAAAA BUILDA BUIL BUCCATGGCT GEGUNTATEC AACCAGCATG COTTGGACTE TATTSYGGGA 120 AGACCOTATT ATTTAAAA ATG OUT CAA CTG AAA TAT ATG GAG AAT GTG GGG Met Ala Glm Leu Lys Tyr Met Glu Asn Val Gly

-55

-50

-60

- 1°

THE GOT CHA GAS GAC AGA GAM CGA ATG CAC AGA ART ATT GTC AGO CTT Tyr Ala win Glu Asp Ard Jaw Arg Met His Arg Ash Ile Val Ser Leu CAA TGC TTC CTC TGG TTT TAC ATT GGT TCT TCA TTG AAT GGT ACT CGG 315

Gln Cys Phe Leu Trp Phe Tyr Ile Gly Ser Ser Leu Asn Gly Thr Arg -15

GGA AAA AGA GTT CCA GCG CAC TTT TCC AAC ACA TCA CTG CAT TAT TTG 363

Gly Lys Arg Val Pro Ala His Phe Ser Asn Thr Ser Leu His Tyr Leu 15

AAT GCA GCA TGG CCG CGG Asn Ala Ala Trp Pro Arg 20

(2) INFORMATION FOR SEQ ID NO: 284:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 293 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 3..294
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 98 region 1..292

id HUM524F05B

est

- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 44..172
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 99

region 48..176

id H81799

est

- (in) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 167..276
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 96

region 170..279

ıd H81799

est

- (12) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 14..43
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 97

region 16..50 id H81799 est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 48..172
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 57..181

id T84779

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 167..226
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93

region 175..234

id T84779

est

(1M) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..45
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 7..51 id T84779

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 167..294
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94

region 101..228

id W81213

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 66..172
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 1..107

id W81213

est

0 - +

::: FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 8..172
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 1..165

1d AA030080

	(C) IDE	NTIFICATION ME ER INFORMATION	: identit	y 93 159202	
(ix)	(B) LOCA	E/KEY: sig_pep ATION: 17426 NTIFICATION ME ER INFORMATION	6 THOD: Von : score 3	Heijne matrix .5 LSTRSGGTHA/CS	
(xi)	SEQUENCE	DESCRIPTION:	SEQ ID NO:	284:	
AAAAACAATA	GGACGGAA	AC GCCGAGGAAC	CCGGCTGAGG	CGGCAGAGCA TCCTG	GCCAG 60
AACAAGCCAF	GGAGCCAA	GA CGAGAGGGAC	ACACGGACAA	ACAACAGACA GAAGA	CGTAC 120
TGGCCGCTGG	ACTCCKCT	GC CTCCCCCATC	TCCCCGCCAT	CTGCGCCCGG AGG A	TG 176
AGC CCA GC Ser Pro Al -30	CC TTC AGG a Phe Arg	GCC ATG GAT G Ala Met Asp V -25	TG GAG CCC al Glu Pro -20	CGC GCC AAA GGS Arg Ala Lys Gly	TCC 224 Ser -15
TTC TGG AG Phe Trp Se	SC CCT TTG er Pro Leu -10	TCC ACC AGG T Ser Thr Arg S	CG GGG GGC er Gly Gly -5	ACT CAT GCG TGC Thr His Ala Cys 1	TCC 272 Ser
GCT TCA AT Ala Ser Me					293
	SEQUENCE ((A) LENG (B) TYPE (C) STR	SEQ ID NO: 28 CHARACTERISTIC STH: 347 base part of the second sec	S: pairs D		
(ii)	MOLECULE	TYPE: CDNA			
(vi)		SOURCE: ANISM: Homo Sa SUE TYPE: Subs		ra	
(1x)	(B) LOCA	E/KEY: other ATION: 26326 RTIFICATION ME ER INFORMATION	THOD: blas	y 99 42342	
	FEATURE:				

- (A) NAME/KEY: other
 (B) LOCATION: 19..345
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 11..337 id AA133412

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(114..345)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 172..403

id AA156940

est

est

(1K) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(71..114)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 402..445

id AA156940

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement (26..76)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92

region 439..489

id AA156940

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 172..345
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 186..359

id W07240

est

(1K) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 72..171
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 83..192

1d W07240

est

(1M) FEATURE:

- :A: UAME/KEY: other
- (B) LOCATION: 21..76
- of company and a second

	(.	ix)	(B)	NAMI LOCA I DEI	E/KE ATION NTIF: ER IN	N: 39	93 ION 1	METH	ide: reg.	plast ntity ion 1 R8101	y 98 L30)7				
	(:	ix)	(B) (C)	NAME LOCA I DEN	OITA	N: 18	317 [ON 1	METHO	DD: 1	Von H re 3. SIL <i>H</i>	. 5					
	()	(i) :	SEQUE	ENCE	DESC	CRIP:	NOIT	: SEÇ	QID	NO:	285	:				
AGC	GCTGA	ACG (CCGA(Glu (Leu A			50
			GCC Ala -40													93
GCC Ala	CAA Gln	CAG Gln -25	GAA Glu	GCA Ala	AAG Lys	CAC His	AGG Arg -20	GAA Glu	GCA Ala	GAA Glu	ATG Met	AGA Arg -15	AAC Asn	AGT Ser	ATC Ile	146
TTA Leu	GCC Ala -10	CAA Gln	GTT Val	CTG Leu	GAT Asp	CAG Gln -5	TCG Ser	GCC Ala	CGG Arg	GCC Ala	AGG Arg 1	TTA Leu	AGT Ser	AAC Asn	TTA Leu 5	194
GCA Ala	CTT Leu	GTA Val	AAG Lys	CCT Pro 10	GAA Glu	AAA Lys	ACT Thr	AAA Lys	GCA Ala 15	GTA Val	GAG Glu	AAT Asn	TAC Tyr	CTT Leu 20	ATA Ile	242
CAG Gln	ATG Met	GCA Ala	AGA Arg 25	TAT Tyr	GGA Gly	CAA Gln	CTA Leu	AGT Ser 30	GAG Glu	AAG Lys	GTA Val	TCA Ser	GAA Glu 35	CAA Gln	GGT Gly	290
TTA Leu	ATA Ile	GAR Glu 40	ATC Ile	CTT Leu	AAA Lys	AAA Lys	GTA Val 45	AGC Ser	CAA Gln	CAA Gln	ACA Thr	GAA Glu 50	AAG Lys	AHN Xaa	ACA Thr	338
	GTG Val 55															347
2;	INF	DRMA'	TION	FOR	SEQ	ID 1	NO: :	286:								

(i) SEQUENCE CHARACTERISTICS:

(D) TOPOLOGY: LINEAR

(A) LEMGTH: 414 base pairs (B) TYPE: MUCLEIC ACID (C) STPANDEDNESS: DOUBLE

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 186..382
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 156..352

1d AA082259

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..146
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93

region 34..119

id AA082259

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 29..61
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96

region 1..33

id AA082259

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 194..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 169..306

id H80945

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 54..146
- (3) IDENTIFICATION METHOD: blastn
- D' "THER INFORMATION: identity 93

region 30..122

id H80945

est

iw: FEATURE:

- TA: MAME/KEY: sig peptide
- # 160ATION: 157..345
- THE THEORY TO THE PROPERTY OF THE PROPERTY OF

AAC.	AGCG	GGC	AGGG.	AAAG	CC G	CGGG.	AAGG	G TA	CTCC	AGGC	GAG	AGGC	GGA	CGCG.	AGTCGT	60
CGT	GG DA	GGA	AAAG	TGAC	TA G	CTCC	CCTT	C GT	TGTC.	AGCC	AGG	GACG.	AGA .	ACAC.	AGCCAC	120
GCT	CCCAI	MCC	GGCT	GCCH.	AA G	RWTC	CCTS	G GC	GGCG	ATG Met				GGT Gly		174
CGA Arg	GGC Gly	CTG Leu -55	CGG Arg	GCC Ala	ACC Thr	TAC Tyr	CAC His -50	CGG Arg	CTC Leu	CTC Leu	GAT Asp	AAA Lys -45	GTG Val	GAG Glu	CTG Leu	222
ATG Met	CTG Leu -40	CCC Pro	GAG Glu	AAA Lys	TTG Leu	AGG Arg -35	CCG Pro	TTG Leu	TAC Tyr	AAC Asn	CAT His -30	CCA Pro	GCA Ala	GGT Gly	CCC Pro	270
AGA Arg -25	ACA Thr	GTT Val	TTC Phe	TTC Phe	TGG Trp -20	GCT Ala	CCA Pro	ATT Ile	ATG Met	AAA Lys -15	TGG Trp	GGG Gly	TTG Leu	GTG Val	TGT Cys -10	318
GCT Ala	GGA Gly	TTG Leu	GCT Ala	GAT Asp -5	ATG Met	GCC Ala	AGA Arg	CCT Pro	GCA Ala 1	GAA Glu	AAA Lys	CTT Leu	AGC Ser 5	ACA Thr	GCT Ala	366
CAA Gin	TCT Ser	GVK Xaa 10	GTT Val	TTG Leu	ATG Met	GCT Ala	ACA Thr 15	GGG Gly	TTT Phe	ATT Ile	TGG Trp	TCA Ser 20	AGA Arg	TAC Tyr	TCG Ser	414

(2) INFORMATION FOR SEQ ID NO: 287:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 478 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Muscle
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 196..391
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 95

region 185..380

id W07314

est

(1x% FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 58..204
- (C) IDENTIFICATION METHOD: blastn
- (3) OTHER INFORMATION: identity 98 region 46..192

id W07314

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 409..478
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 401..470

id W07314

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 34..412
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 12..390

id W07582

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 45..393
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 31..379

id W73850

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 16..52
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94

region 1..37

id W73850

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 73..447
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 1..375

id AA112776

est

(1x) FEATURE:

- A' MAME/KEY: other
- Le LOCATION: 63..388
- 13 IDENTIFICATION METHOD: blastn
- OTHER INFORMATION: identity 99

region 1..326

ıd H72671

est

seq TGXLNMTLQRASA/AP

(xi) SEQUENCE DESCRIPTION: SEQ.ID NO: 287:

AACTTGTCAG CCCTTG	TCTG AGGCGGAGGC A	GCCCCGCGC CGCGCCGGAC	CCGAGCATAT 60
TTCATTTTCT GTCATT	GGAC TTTGAGCCAT T	AGAACC ATG AGC AAC TA Met Ser Asn Ty -85	
TCA CTG GTT GGC Co Ser Leu Val Gly P -80	CA GCT CCT TGG GG ro Ala Pro Trp Gl -75	T TTC CGG CTG CAG GGC y Phe Arg Leu Gln Gly -70	GGT AAG 163 Gly Lys -65
Asp Phe Asn Met P.	CT CTG ACA ATC TC ro Leu Thr Ile Se 60	T AGT CTA AAA GAT GGC r Ser Leu Lys Asp Gly -55	GGC AAG 211 Gly Lys -50
GCA GCC CAG GCA AMARIA	AT GTA AGA ATA GG sn Val Arg Ile Gl -4	C GAT GTG GTT CTC AGC y Asp Val Val Leu Ser 0 -35	ATT GAT 259 Ile Asp
GGA ATA AAT GCA CA Gly Ile Asn Ala G -30	AA GGA ATG ACT CA ln Gly Met Thr Hi: -25	I CTT GAA GCC CAG AAT s Leu Glu Ala Gln Asn -20	AAG ATT 307 Lys Ile
AAG GGT TGT ACA GG Lys Gly Cys Thr G: -15	GA NYT TTG AAT ATO ly Xaa Leu Asn Me -10	G ACT CTG CAA AGA GCA t Thr Leu Gln Arg Ala -5	TCT GCT 355 Ser Ala
GCA CCC AAG CCT GA Ala Pro Lys Pro G	AG CCG GTT CCT GT lu Pro Val Pro Va. 5	I CAA AAG CCC ACA GTC l Gln Lys Pro Thr Val 10	ACC AGC 403 Thr Ser 15
GTG TGT TCC GAG AG Val Cys Ser Glu Th 20	CT TCT CAG GAG CT hr Ser Gln Glu Le 2	A GCA GAG GGA CAG AGA u Ala Glu Gly Gln Arg 5 30	AGA GGA 451 Arg Gly
TOO CAG GGT GAC AC Ser Gln Gly Asp Se 35			478

(2) INFORMATION FOR SEQ ID NO: 288:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 355 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - F) TISSUE TYPE: Uterus
- (ix) FEATURE:
 - (A) NAME/KEY: other

- (P) LOCATION: 4..333
- (3) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 1..330 id N35568 est

(ix) FEATURE:

- (A) NAME/KEY: other
- (5) LOCATION: 26..297
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 1..272

id R35915

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (P) LOCATION: 295..338
- (C) IDENTIFICATION METHOD: blastn
- (E) OTHER INFORMATION: identity 100

region 271..314

id R35915

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 44..255
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 1..212

id W31312

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 251..355
- (C) IDENTIFICATION METHOD: blastn
- OTHER INFORMATION: identity 98

region 209..313

id W31312

est

(ix) FEATURE:

- (A) NAME/KEY: other
- 8) LOCATION: 21..328
- DESCRIPTION OF THE PROPERTY OF
- 07 = OTHER INFORMATION: identity 99

region 13..320

id HSC1MA011

est

CIR HARTURE:

- (A) NAME/KEY: other LOCATION: 62..339
- 1 DENTIFICATION METHOD: blastn
 2THEP IMPORMATION identity 32

<pre>(ix) FEATURE: (A) NAME/KEY: sig_peptide (B) LOCATION: 245298 (C) IDENTIFICATION METHOD: Von Heijne matrix (D) OTHER INFORMATION: score 3.5</pre>	
seq LLGLELSEAEAIG/AD	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:	
ATTOGTTTAC AGTTCGGCAC GTAGGACGGA GGGTAGTGCG TCTAGAGACA CATATTCCCA	60
ACGGATTTGA CGATGGTGTT CGGTCTTGAA TGGAAATGTA GTCTTAGGCC AGTCTTAGGT	120
TTTTGAACAG GATAGTAGGT ATCCGGAGTC GATTGAGGGC CAGAGCAGGC ACTGGGGTTC	180
GGATCCTGGG CAAAGTTTCC CACATTGAGG GTCTCGAGGA CGCCTAGATC TCTTTCCCAG	240
GGCC ATG GCG AAC CCG AAG CTG CTG GGA CTG GAG CTA AGC GAG GCG GAG Met Ala Asn Pro Lys Leu Leu Gly Leu Glu Leu Ser Glu Ala Glu -15 -10 -5	289
GCG ATC GGT GCT GAT TCG GCG CGA TTT GAG GAG CTG CTG CAG GCC Ala Ile Gly Ala Asp Ser Ala Arg Phe Glu Glu Leu Leu Gln Ala	337
TCG AAG GAG CTC CAG CAA Ser Lys Glu Leu Gln Gln 15	355
(2) INFORMATION FOR SEQ ID NO: 289:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 401 base pairs (B) TYPE: NUCLEIC ACID (C) STRANDEDNESS: DOUBLE (D) TOPOLOGY: LINEAR	
(ii) MOLECULE TYPE: CDNA	
<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo Sapiens (D) DEVELOPMENTAL STAGE: Fetal (F) TISSUE TYPE: brain</pre>	
(in) FEATURE: (A) NAME/KEY: other (B) LOCATION: 113201 (C) IDENTIFICATION METHOD: blastn (D) OTHER INFORMATION: identity 100 region 90178 id W21198 est	
(im FEATURE: (A) NAME/KEY: other (A) LOCATION: 2374	

(C) IDENTIFICATION METHOD: blastn (D) OTHER INFORMATION: identity 98

region 2..53 id W21198 est

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 71..111
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 49..89

id W21198

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (E) LOCATION: complement(114..201)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94

region 271..358

id AA061731

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(114..201)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94

region 271..358

id AA061768

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (3) LOCATION: complement(125..201)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96

region 269..345

id AA058174

est

Viks FEATURE:

- (A) NAME/KEY: sig peptide
- (B) LOCATION: 204..323
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5

seq ALLCTLLLHFQNI/RR

TENUENCE DESCRIPTION: SEQ ID NO: 289:

AAAGSTEL , GGATGGGAGG GAGGTTCGGG TGGGCATCGG GGGGCTGGAA GAGCTCGAGT 60

GGTCCTGLE GGAAAGCGCG AGTCTGAGTG GAACCCTGGA CGACTTGCAG AGCGGCTGGC 120

HUART HATE UNGGACTACTO GAAGTCACAS CCAAAGAAAT TOTSTGATTA CTGCAAGTGO 180

TO MATERIAL STATE TO THE TOTAL THE TANK AND THE STATE AND

Ile Ile Val Leu Asn Glu Val Leu Leu Phe Asp Val Asn Ser Val Tyr -20

AAA GCA CTT TTA TGT ACA TTG CTC TTG CAT TTT CAA AAC ATC AGA AGA Leu Leu Cys Thr Leu Leu His Phe Gln Asn Ile Arg Arg 1

TTT CTG TCT TCT CAG TCC CCT ATG AAA GCT GTG AGC CTT CTA THT TTT Phe Leu Ser Ser Gln Ser Pro Met Lys Ala Val Ser Leu Leu Xaa Phe 10

CAT CAA CCT GAC TTT GAT TAT ATA His Gln Pro Asp Phe Asp Tyr Ile 20

AAA GCA CTT TCT GAT TAT ATA 11e 25

(2) INFORMATION FOR SEQ ID NO: 290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..382
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 97 region 4..337

id HUMGPCRB

vrt

(1X) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 292..345
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98 region 1..54

region 1..5 id T29782

est

(im) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 345..382
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94

region 55..92

id T29782

est

De FEATURE:

/A) NAME/KEY: sig_peptide

(B) LOCATION: 80..235

(0)	IDENTI	FICATION	METHO	DD:	Von	Heijne	matrix
(D)	OTHER	INFORMAT	ION:	sco	re 7	7.4	
				șeg	LVE	FIIGLVG	NLLA/LV

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

AACTTCAGTT T	GGACAACTA CTCA	CAGCTA CTACAC	AGAG ACCCGAACGA GTC	ACTGATA 60
TADACCTGGA C			G GCA AAC AAT TTT AC t Ala Asn Asn Phe Ti -45	
		y Asn Asp Cys	GAC CTC TAT GCA CAT Asp Leu Tyr Ala His -30	
			TAC AGC CTC GTC TTC Tyr Ser Leu Val Phe	
			GTC GTC ATT GTT CAP Val Val Ile Val Glr 5	
			TCA ACA AAT TTG GTT Ser Thr Asn Leu Val 20	
		r Ala Leu Pro	ACA CGA ATA GCT ACT Thr Arg Ile Ala Thr 35	
	TTG ACT GGA GA Leu Thr Gly Gl 45			385

(2) INFORMATION FOR SEQ ID NO: 291:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (3) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (0) TOPOLOGY: LINEAR

: MOLECULE TYPE: CDNA

"" DRIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Pancreas

.: FEATURE:

AAR NAME/KEY: other E) LOCATION: 55..462

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 47..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 1..218

id W77946 est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 263..412
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 216..365

id W77946

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 412..462
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 366..416

id W77946

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 54..462
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 1..409

id C16991

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 263..462
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 212..411

id N28784

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 52..214

id N28784

est

.im. FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..107
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100 region 1..58

id N28784 est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 54..356
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 1..303 id C17735

est

(1x) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 357..462
- (3) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 303..408

id C17735

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96

region 47..209

id AA057588

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 263..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 207..350

id AA057588

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 406..462
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 351..407

id AA057598

est

. H FEATURE:

- (A) NAME/KEY: other
- (3) LOCATION: 55..107
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100 region 1..53

id AA057588

est

(D) OTHER INFORMATION: score 7 seq SMIGIGSLPSCWA/CW (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291: AGTTCGTTTA TTCCTCCGCG CGCTGGGACA GGCTGCTTCT TCGCCAGAAC CAACCGGTTG CTTGCTGTCC CAGCGGCGCC CCCTCATCAC CGTCGCCATG CCCGGAGGTC TGCTTCTCGG GGACGTGGCT CCCAACTTTG AGGCCAATAC CACCGTCGGC CGCATCCGTT TCCACGACTT TCTGGGAKAC TCATGGGGCA TTCTCTTCTC CCACCCTCGG GACTTTACCC CAGTGTGCAC 240 CACAGAGCTT GGCAGAGCTG CAAAGCTGGC ACCAGAATTT GCCAAGAGGA ATGTTAAGTT 300 GWTTGCCCTT TCAATAGACA GTGTTGAGGA CCATCTTGCC TGGAGCAAGG ATATCA ATG 359 CTT ACA ATT GTG AAG AGC CCA CAG AAA AGT TAC CTT TTC CCA TCA TCG 407 Leu Thr Ile Val Lys Ser Pro Gln Lys Ser Tyr Leu Phe Pro Ser Ser -25 -20 ATG ATA GGA ATC GGG AGC TTG CCA TCC TGT TGG GCA TGC TGG ATC CAG 455 Met Ile Gly Ile Gly Ser Leu Pro Ser Cys Trp Ala Cys Trp Ile Gln -10 -5 CAG AGA 461 Gln Arg 5 (2) INFORMATION FOR SEO ID NO: 292: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 69 amino acids (B) TYPE: AMINO ACID (D) TOPOLOGY: LINEAR (ii) MOLECULE TYPE: PROTEIN (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo Sapiens (F) TISSUE TYPE: Liver (ix) FEATURE: (A) NAME/KEY: sig_peptide (B) LOCATION: -35..-1 (C) IDENTIFICATION METHOD: Von Heijne matrix (D) OTHER INFORMATION: score 15

Met Ser Ser Trp Ser Arg Gln Arg Pro Lys Ser Pro Gly Gly Ile Gln -35 -25 -20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

seq LFLLLLLAASAWG/VT

Pro His Val Ser Arg Thr Leu Phe Leu Leu Leu Leu Leu Ala Ala Ser -15 -10 -5 Ala Trp Gly Val Thr Leu Ser Pro Lys Asp Cys Gln Val Phe Arg Ser 1 5 . 10

Asp His Gly Ser Ser Ile Ser Cys Gln Pro Pro Ala Glu Ile Pro Gly
15 20 25

Tyr Leu Pro Ala Thr

2: INFORMATION FOR SEQ ID NO: 293:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (V1) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Hypertrophic prostate
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -21..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 13.2 seq LLLXAVLLSLASA/SS
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:
- Met Arg Val Arg Ile Gly Leu Thr Leu Leu Leu Xaa Ala Val Leu Leu -20 -15 -10
- Ser Leu Ala Ser Ala Ser Ser Asp Glu Glu Gly Ser Gln Asp Glu Ser
 -5 1 5 10
- Leu Asp Ser Lys Thr Thr Leu Thr Ser Asp Glu Ser Val Lys Asp His
 15 20 25
- Thr Thr Ala Gly Arg Val Val Ala Gly Gln Ile Phe Leu Asp Ser Glu 30 35 40
- Fig. Ser Glu Leu Glu Kaa Ser Ile Gln Glu Glu Glu Asp Ser Leu Lys 50 55
- Ser A.n Glu Gly Glu Ser Val Thr Glu Asp Ile Ser Phe Leu Glu Ser

. THE EMETION FOR "SQ ID NO: 294:

- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Substantia nigra
- (1K) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -21..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 13.1

seq CVLLLLLLTRS/SE

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:
- Met Phe Ser His Leu Pro Phe Asp Cys Val Leu Leu Leu Leu Leu Leu -20 -15 -10
- Leu Leu Thr Arg Ser Ser Glu Val Glu Xaa Xaa Ala Glu Val Gly Gln -5 1 5 10
- Asn Ala Tyr Leu Pro Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu 15 20 25
- Val Pro Val Cys Trp Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly 30 35 40
- Asn Val Val Leu Arg Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser 45 50 55
- Arg Tyr Trp Leu Asn Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr 60 70 75
- Ile Glu Asn Val Thr Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile 80 85 90
- Gln Ile Pro Gly Ile Met Asn Asp Glu Lys Phe Asn Leu 95 100
- (2) INFORMATION FOR SEQ ID NO: 295:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TGPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
 - (1x) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -21..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix

- (D) OTHER INFORMATION: score 11.6 seq LLFLFLAVDEAWA/GM
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

Met 31y Pro Val Arg Leu Gly Ile Leu Leu Phe Leu Phe Leu Ala Val -20 -15 -10

Amp Glu Ala Trp Ala Gly Met Leu Lys Glu Glu Gly Arg

- (2) INFORMATION FOR SEQ ID NO: 296: -
 - (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Kidney
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -17..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 10.7 seq SLLLAVALGLATA/VS
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:
- Not Lys Ser Leu Ser Leu Leu Leu Ala Val Ala Leu Gly Leu Ala Thr
 -15 -10 -5
- Aia Val Ser Ala Gly Pro Ala Val Ile Glu Cys Trp Phe Val Glu Asp 1 5 10 15
- Ala Ser Gly Lys Gly Leu Ala Lys Arg Pro Gly Ala Leu Leu Leu Arg
 20 25 30
- of Bly Pro Gly Did Pro Pro Pro Arg Pro Asp Leu Asp Pro Glu Leu 40 45
- Two Dec Ser Vol Him Asp Pro Ala Gly Ala Leu Gln Ala Arq 50 55 60

IMPORMATION FOR SEQ ID NO: 297:

THITTE HARACTERISTICS.

- (11) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TYSSUE TYPE: Hypertrophic prostate
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -16..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 9.6

seq LLTLXLLGGPTWA/GK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

Met Leu Leu Leu Thr Leu Xaa Leu Leu Gly Gly Pro Thr Trp Ala
-15 -5

Gly Lys Met Tyr Gly Pro Gly Gly Gly Lys Tyr Phe Ser Thr Thr Glu
1 5 10 15

Asp Tyr Asp His Glu Ile Thr Gly Leu Arg Val Ser Val Gly Leu Leu 20 25 30

Leu Val Lys Ser Val Gln Val Lys Leu Gly Asp Ser Trp Asp Val Lys
35 40 45

Leu Gly Ala Leu Xaa Gly Asn Thr Gln Glu Val Xaa Xaa Gln Pro Gly 50 55 60

Glu Tyr Ile Thr Lys Val Phe Val Ala Phe Gln Ala Phe Leu Arg Gly
65 70 75 80

Met Val Met Tyr Thr Ser Lys Asp Arg 85

- (2) INFORMATION FOR SEQ ID NO: 298:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Cancerous prostate
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -46..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 9.4 seq LIILIXIWIWCLG/SO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

Met Lys Ile Gly Ile Leu Leu Ser Leu Leu Asn Ser Val Ile Ser Gln -45 . -35

Thr Leu Met Ser Cys Asn Trp Lys Gln Gln Met Arg Arg Met Lys Thr -30 -25 -20 -15

Ile Leu Ile Leu Ile Xaa Ile Trp Ile Trp Cys Leu Gly Ser Gln
-10 -5 1

The Phe Gly The Ser The The Lys Ser Val Gln Leu Lys Ile Leu Arg
5 10 15

Gln Asn Leu Ser His Phe Leu Gln Pro Pro Gln Val Ile 20 , 25 30

12 INFORMATION FOR SEQ ID NO: 299:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 94 amino acids
 - (3) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (11) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
- (1x) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -30..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 9.4

seq LPFLLSLFPGALP/VQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

Met Lys Ala Ser Ser Gly Arg Cys Gly Leu Val Arg Trp Leu Gln Val -30 -25 -20 -15

Le: Leu Pro Fhe Leu Leu Ser Leu Phe Pro Gly Ala Leu Pro Val Gln

1.6 Arg Tyr Jar He Pro Glu Glu Leu Ala Lys Asn Ser Val Val Gly

Act. Led Ald Lys Asp Leu Gly Leu Ser Val Arg Asp Leu Pro Ala Arg

Lys Leu Arg Tal Sor Ala Glu Lys Glu Tyr Phe Thr Val Asn Pro Glu 40 45 50

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- (2) INFORMATION FOR SEQ ID NO: 300:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Normal prostate
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -33..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 9.1

seq IIFLCHLLRGLHA/XT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

Met Ile Val Asp Cys Val Ser Ser His Leu Lys Lys Thr Gly Asp Gly
-30 -25 -20

Ala Lys Thr Pne Ile Ile Phe Leu Cys His Leu Leu Arg Gly Leu His
-15 -10 -5

Ala Xaa Thr Asp Arg Glu Lys Asp Pro Leu Met Cys Glu Asn Ile Gln
1 5 10 15

Thr His Gly Arg Leu Pro 20

- (2) INFORMATION FOR SEO ID NO: 301:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 109 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - TISSUE TYPE: Ovary
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (F) LOCATION: -104..-1
 - (3) IDENTIFICATION METHOD: Von Heijne matrix
 - OTHER INFORMATION: score 9.1

seq LTSLSWLLXASCS/KP

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

Met Ala Lys Ala Leu Leu Phe Pro Ser Gly Arg Ser Val Arg Val Leu

-90

-100

-95

Tyr Gly Ala Val Asn Lys Glu Arg Gln Xaa Glu Ser Val Leu Asn Arg
-85 -80 -75

Ala Cys Pro Pro Lys Ala Asn Ser Lys Glu Arg Arg Gly Arg Ala Val -70 -65 -60

Led Gly Ala Glu Leu Thr Gln Trp Ser Ser Pro Thr Thr Ala Gly Ser
-55 -50 -45

Cys Cys Ser Ser Cys Thr Leu Cys Ala Arg Ser Ser Ser Xaa Val Ile
-40 -35 -30 -25

Ala Pro Ser Pro Leu Val Pro Phe Thr Ser Gly Leu Thr Ser Leu Ser -20 -15 -10

Trp Leu Leu Xaa Ala Ser Cys Ser Lys Pro Xaa Lys Gly
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 302:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 134 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
- (ix) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -73..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 8

seg LATKLLSLSGVFA/VH

- (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 302:
- Mot Ala Al: Ser Glu Ala Ala Val Val Ser Ser Pro Ser Leu Lys Thr
- Asp Throws as a Val Leu Glu Thr Ala Gly Thr Val Ala Ala Met Ala -50 -45
- Ala Thr Pro dor Ala Arg Ala Ala Ala Ala Val Val Ala Ala Ala Ala -40 -35 -30
- And The \mathbb{R}^2 is the Ala Arq Val Ser Lys Ala Ala Leu Ala The Lys -20 in -15

20

10

Ala Gly Met Pro Ser Pro Glu Trp Thr Xaa Arg Lys Lys Gln Thr Xaa 25 30 35

15

Glu Asn Trp Ala Trp Arg Asp Ser Arg Gln Arg Xaa Arg Gly Val Leu 40 50 55

Val Val Gly Ile Gly Ala 60

- (2) INFORMATION FOR SEQ ID NO: 303:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -17..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 7.8

seq VLWLISFFTFTDG/HG

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:
- Met Lys Val 3ly Val Leu Trp Leu Ile Ser Phe Phe Thr Phe Thr Asp -15 -5
- Gly His Gly Gly Phe Leu Gly Val Ser Trp Cys Tyr Val Ser Tyr Leu 1 5 10

Phe Ser Thr Asn Ser Pro Leu Ser Phe Arg Arg Met 20 25

- (2) INFORMATION FOR SEQ ID NO: 304:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 119 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii: MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Surrenals

- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -19..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 7.4 seq WIFLAAILKGVQC/EV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

Mot Glu Pne Gly Leu Ser Trp Ile Phe Leu Ala Ala Ile Leu Lys Gly
-15
-10
-5

Fro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe
15 20 25

Thr Asp Ala Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu 30 45

Glu Trp Val Ala Asn Ile Xaa Ser Thr Ala Ser Gly Gly Thr Arg Gly
50 55 60

Tyr Ala Ala Pro Val Lys Asp Arg Phe Ile Ile Ser Arg Asp Asp Ser
65 70 75

Arg Asn Thr Leu His Leu Gln Met Asn Gly Leu Lys Xaa Met Thr Gln 80 85 90

Ala Ile Tyr Tyr Cys Ala Thr 95 100

- (2) INFORMATION FOR SEQ ID NO: 305:
 - (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 150 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - FIRST OFIGINAL SOURCE:
 - A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Cancerous prostate
 - 1 Km FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -37..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 7.4 seq LWRLLLWAGTAFQ/VX

 σ^{\otimes} upwide description, sec to we see

- Arg Thr Glu Arg Arg Ile Pro Arg Leu Trp Arg Leu Leu Leu Trp Ala -20 -15 -10
- Gly Thr Ala Phe Gln Val Xaa Gln Gly Xaa Xaa Pro Glu Leu Xaa Ala -5 10
- Cys Lys Glu Ser Glu Tyr His Tyr Glu Tyr Thr Ala Cys Asp Ser Thr
 15 20 25
- Gly Ser Arg Trp Arg Val Ala Val Pro His Thr Xaa Gly Leu Cys Thr 30 40
- Ser Leu Pro Asp Pro Val Lys Gly Thr Glu Cys Xaa Xaa Ser Cys Asn 45 50 55
- Ala Gly Glu Phe Leu Asp Met Lys Asp Gln Ser Cys Xaa Pro Cys Ala 60 65 70 75
- Glu Gly Arg Tyr Ser Leu Gly Thr Gly Ile Arg Phe Asp Glu Trp Asp 80 85 90
- Glu Leu Pro His Gly Phe Ala Ala Ser Gln Pro Thr Trp Ser Trp Met $95 \hspace{1.5cm} 100 \hspace{1.5cm} 105 \hspace{1.5cm}$

Thr Val Leu Leu Ser His

(2) INFORMATION FOR SEQ ID NO: 306:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Umbilical cord
- (ix) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -25..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 7.1
 - seq QACLLGLFALILS/GK
- (M1) SEQUENCE DESCRIPTION: SEQ ID NO: 306:
- Met Thr Ala Asp Pro Arg Lys Gly Arg Met Gly Leu Gln Ala Cys Leu -25 -15 -10
- Leu Gly Leu Phe Ala Leu Ile Leu Ser Gly Lys Cys Ser Xaa Ser Pro
 +5 1 5
- Glu Pro Asp Gln Arg Arg Thr Leu Pro Pro Gly Trp Val Ser Leu Gly
 15 20

Arg Ala Asp Pro Glu Glu Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln 25 30 . 35

Gln Asn Val Glu Arg Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro 40 45 50 55

Ser Ser Pro Sln Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp
60 65 70

Leu Val Arg Pro Ser Pro Leu Thr Pro 75 80

(2) INFORMATION FOR SEQ ID NO: 307:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (11) MOLECULE TYPE: PROTEIN
- (v1) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -24..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 6.9 seq LCFLLLAVAMSFF/GS
- MAI SEQUENCE DESCRIPTION: SEQ ID NO: 307:

Met Leu Val Asp Gly Pro Ser Glu Arg Pro Ala Leu Cys Phe Leu Leu -20 -15 -10

Leu Ara Val Ala Met Ser Phe Phe Gly Ser Ala Leu Ser Ile Asp Glu
-5

Thr Ang Ang His Leu Leu Leu Lys Xaa Lys Met Met Arg Leu Gly Gly

In: Led And Ile Ala Glu Met Lys Glu Ala Met Arg Thr Leu Ile Phe 45 50 55

Fro Fig. 2- p Met His Phe Phe

- (A) LENGTH: 128 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -17..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 6.8

seq LVLVLVVAVTVRA/AL

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:
- Met Ala Ala Pro Leu Val Leu Val Leu Val Val Ala Val Thr Val Arg -15 -10 -5
- Ala Ala Leu Phe Arg Ser Ser Leu Ala Glu Phe Ile Ser Glu Arg Val 1 5 10 15
- Glu Val Val Ser Pro Leu Ser Ser Trp Lys Arg Val Val Glu Gly Leu 20 25 30
- Ser Leu Leu Asp Leu Gly Val Ser Pro Tyr Ser Gly Ala Val Phe His 35 40 45
- Glu Thr Pro Leu Ile Ile Tyr Leu Phe His Phe Leu Ile Asp Tyr Ala
 50 60
- Glu Leu Val Phe Met Ile Thr Asp Ala Leu Thr Ala Ile Ala Leu Tyr
 65 70 75
- Phe Ala Ile Gln Asp Phe Asn Lys Val Val Phe Lys Lys Gln Lys Leu 80 85 90 95
- Leu Leu Glu Leu Asp Gln Tyr Ala Pro Asp Val Ala Glu Leu Ile Arg 100 105 110
- (2) INFORMATION FOR SEQ ID NO: 309:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 132 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Substantia nigra
 - (133) FEATURE:
 - (A) NAME/KEY: sig_peptide

- (B) LOCATION: -102..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7 seq LXMTLMLPFKILS/DS
- (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

Met Inr Ala Ala Ile Arg Arg Gln Arg Glu Leu Ser Ile Leu Pro Lys -100 -95 -90

Val Thr Leu Glu Ala Met Asn Thr Thr Val Met Gln Gly Phe Asn Arg -85 -80 -75

Ser Glu Arg Cys Pro Arg Asp Thr Arg Ile Val Gln Leu Val Phe Pro -70 -65 -60 -55

Ala Leu Tyr Thr Val Val Phe Leu Thr Gly Ile Leu Leu Asn Thr Leu
-50 -45 -40

Als Dau Trp Val Phe Val His Ile Pro Ser Ser Ser Thr Phe Ile Ile
-35 -30 -25

Ty: Leu Lys Asn Thr Leu Val Ala Asp Leu Xaa Met Thr Leu Met Leu -20 -15 -10

Pro Phe Lys Ile Leu Ser Asp Ser His Leu Ala Pro Trp Gln Leu Arg
-5 1 5 10

Ala Phe Val Cys Arg Phe Ser Ser Val Ile Phe Tyr Glu Thr Met Tyr
15 20 25

Val Gly Glu Gly

(2) INFORMATION FOR SEQ ID NO: 310:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (11) MOLECULE TYPE: PROTEIN
- .vi= ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Spleen
- (1) (EATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -46..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - O' OTHER INFORMATION: score 6.3

seq SIGVLTLSHLISG/LR

-35

- 4.5

-40

Ala Gly Thr Pro Gly Ile Ser Glu Lys Asp Asn Arg Asp Pro Ala Gly
-30 -20 -15

Ser Ser Ile Gly Val Leu Thr Leu Ser His Leu Ile Ser Gly Leu Arg -10 -5 l

Thr Leu Tyr Thr Leu Leu His Phe Pro Leu Arg
5 10

(2) INFORMATION FOR SEQ ID NO: 311:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Thyroid
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -50..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 6.3

seq LIILGLVLFMVYG/NV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

Men Gly Leu Ala Met Glu His Gly Gly Ser Tyr Ala Arg Ala Gly Gly -35 -40 -35

Ser Ser Arg Gly Cys Trp Tyr Tyr Leu Arg Tyr Phe Phe Leu Phe Val -30 -25 -20

Ser Leu Ile Gln Phe Leu Ile Ile Leu Gly Leu Val Leu Phe Met Val -15 -5

Tyr Gly Asn Val His Val Ser Thr Glu Ser Asn Leu Gln Ala Thr Glu $1 \hspace{1cm} 5 \hspace{1cm} 10$

Ar; Arg Ala Glu Gly Leu Tyr Xaa Gln Leu Leu Gly Leu Thr Ala Ser 1 20 25 30

Gl: Ser Asn Leu Thr Lys Glu Leu Asn Phe Thr Thr Arg Ala Lys Asp
35 40 45

Al. The Met Gln Met Trp Leu Asn Ala 50 55

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- ALL' MOLECULE TYPE: PROTEIN
- (V1) OBIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Cancerous prostate
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -64..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 6.3

seq SCLVSGWGLLANG/QR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro -60 -55 -50

Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser
-45 -40 -35

Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr
-30
-25
-20

Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly
-15 -10 -5

Gln Arg

2] INFORMATION FOR SEQ ID NO: 313:

- (:) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 142 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- VI) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Cancerous prostate
- IR: FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -47..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - .03) OTHER INFORMATION: score 6.3

Met Gly Gly Lys Gln Arg Asp Glu Asp Asp Glu Ala Tyr Gly Lys Pro-45 -40 -35

Val Lys Tyr Asp Pro Ser Phe Arg Gly Pro Ile Lys Asn Arg Ser Cys
-30
-25
-20

Thr Asp Val Ile Cys Cys Val Leu Phe Leu Leu Phe Ile Leu Gly Tyr -15 -5 1

Ile Val Val Gly Ile Val Ala Trp Leu Tyr Gly Asp Pro Arg Gln Val 5 10 15

Leu Tyr Pro Arg Asn Ser Thr Gly Ala Tyr Cys Gly Met Gly Glu Asn 20 25 30

Lys Asp Lys Pro Tyr Leu Leu Tyr Phe Asn Ile Phe Ser Cys Ile Leu 35 40

Ser Ser Asn Ile Ile Ser Val Ala Glu Asn Gly Leu Gln Cys Pro Thr 50 60 65

Pro Gln Val Cys Val Ser Ser Cys Pro Glu Asp Pro Trp Thr Xaa Xaa 70 75 80

Lys Thr Ser Ser His Arg Leu Leu Gly Lys Ser Ser Ile Gln 85 90 95

(2) INFORMATION FOR SEQ ID NO: 314:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 120 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Hypertrophic prostate
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -18..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 6.3 seq VLLFLAWVCFLFY/AG
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

Met Gln Lys Ala Ser Val Leu Leu Phe Leu Ala Trp Val Cys Phe Leu
-15 -10 -5

Pao Tyr Ala Gly Ile Ala Leu Phe Thr Ser Gly Phe Leu Leu Thr Arg

1 5 10

Lou Glu Leu Thr Asn His Ser Ser Cys Gln Glu Pro Pro Gly Pro Gly 20 25 30

Ser Leu Pro Trp Gly Ser Gln Gly Lys Pro Gly Ala Cys Trp Met Ala 35 40 45

Ser Arg Phe Ser Arg Val Val Leu Val Leu Ile Asp Ala Leu Arg Phe 50 55 60

Asp Phe Ala Gln Pro Gln His Ser His Val Pro Arg Glu Pro Pro Val 65 70 75

Ser Leu Pro Phe Leu Gly Lys Leu Ser Ser Leu Gln Arg Ile Leu Glu 80 85 90

ile Gln Pro His His Ala Arg Leu 95 100

(2) INFORMATION FOR SEQ ID NO: 315:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (i1) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Lung
- (ix) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -81..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.7

seq CWMMLLGSXGSFL/AP

- (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 315:
- Net Ser Pro Val Leu His Phe Tyr Val Arg Pro Ser Gly His Glu Gly
 -30 -75 -70
- Ala Ala Ser Gly His Thr Arg Arg Lys Leu Gln Gly Lys Leu Pro Glu ± 65 ± 60 ± 55 ± 50
- 19. Glr. Gly Val Glu Thr Glu Leu Cys Tyr Asn Val Asn Trp Thr Ala -45 -40 -35
- -30 -25 Leu Pro Ser Ala Glu Glu Thr Lys Lys Leu Met Trp Leu Phe
- Ty Tys Pro Tyr Cys Trp Met Met Leu Leu Gly Ser Xaa Gly Ser Phe
 -15 -10 -5
- . A. Fire Met Thr Cys Xaa Trp Arg Ser

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (11) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -36..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.6 seq ILRLLGSLSNAYS/PR
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:
- Met Asp Val Thr Pro Arg Glu Ser Leu Ser Ile Leu Val Val Ala Gly
 -35
 -30
 -25
- Ser Gly Gly His Thr Thr Glu Ile Leu Arg Leu Leu Gly Ser Leu Ser -20 -15 -10 -5
- Asn Ala Tyr Ser Pro Arg His Tyr Val Ile Ala Asp Thr Asp Glu Met

 1 5 10
- Ser Ala Asn Lys Ile Asn Ser Phe Glu Leu Asp Arg Ala Asp Arg Asp 15 20 25
- Pro Ser Asn Met Tyr Thr Lys Tyr Tyr Ile His Arg Asn Gly 30 35 40
- (2) INFORMATION FOR SEQ ID NO: 317:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
 - (ix) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -21..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.6 seq LLRVLNLPHNSIG/CV
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

Met Met Gly Val Ala Lys Leu Thr Leu Leu Arg Val Leu Asn Leu Pro $-20 \hspace{1.5cm} -15 \hspace{1.5cm} -10$

His Asn Ser Ile Gly Cys Val Glu Gly Leu Lys Glu Leu Val His Leu $-\mathbb{S}$ 1 5 10

Glu Trp Leu Asn Leu Ala Gly Asn Asn Leu Lys Ala Met Glu Gln Xaa 15 20 25

Asn Ser Cys Thr Ala Leu Gln His Leu Asp 30 35

(2) INFORMATION FOR SEQ ID NO: 318:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 65 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (11) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -36..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.6 seq ILRLLGSLSNAYS/PR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

Met Asp Val Thr Pro Arg Glu Ser Leu Ser Ile Leu Val Val Ala Gly
-35 -30 -25

Ser Gly Gly His Thr Thr Glu Ile Leu Arg Leu Leu Gly Ser Leu Ser -20 -15 -10 -5

Ash Ala Tyr Ser Pro Arg His Tyr Val Ile Ala Asp Thr Asp Glu Met

Als Abn Lys Ile Ash Ser Phe Glu Leu Asp Ard Ala Asp Arg Asp Is 25

×

- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Colon
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -13..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.5

seq MVLLTMIARVADG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

Met Val Leu Leu Thr Met Ile Ala Arg Val Ala Asp Gly Leu Pro Leu -10 -5 1

Ala Ala Ser Met Gln Glu Glu Val Arg Thr Ala Pro Arg Ala Leu
5 10 15

- (2) INFORMATION FOR SEQ ID NO: 320:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Cancerous prostate
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -47..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.3

seq GCGMFTFLSSVXA/AV

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:
- Met Val Pro Val Glu Asn Thr Glu Gly Pro Ser Leu Leu Asn Gln Lys -45 -40 -35
- Gly Thr Ala Val Glu Thr Glu Gly Xaa Gly Ser Arg His Pro Pro Trp
 -30 -25 -20
- Ala Arg Gly Cys Gly Met Phe Thr Phe Leu Ser Ser Val Xaa Ala Ala -15 -5 1
- Val Ser Gly Leu Leu Val Gly Tyr Glu Leu Gly Ile Ile Ser Gly Ala
 5 10 15
- Leu Leu Glm Ile Lys Thr Leu Leu Ala Xaa Ser Cys His Glu Glm Glu

20

25 30

Met Val Val Ser Ser Leu Val Ile Gly .

- (2) INFORMATION FOR SEO ID NO: 321:
 - (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (11) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Cancerous prostate
 - (ix) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -24..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.2

seq LLFPVGRSWSCFA/QT

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:
- Met Glu Thr Phe Leu Glu Pro Asn Asn Lys Lys Leu Leu Phe Pro Val
- Gly Arg Ser Trp Ser Cys Phe Ala Gln Thr Xaa Ser Leu Ala Lys Tyr
- Ile Pro Tyr Ser Leu Trp Lys Tyr Ser Val Leu Ser Gly His Ser 10
- (2) INFORMATION FOR SEQ ID NO: 322:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 110 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - TI: MÜLECULE TYPE: PROTEIN
 - (v1) OFIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Normal prostate
 - (ix) FEATURE:
 - A: NAME/KEY: sig_peptide
 - P IOCATION: -15 -1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

Met Gly Phe Leu Trp Gly Leu Ala Leu Pro Leu Phe Phe Cys Trp
-15 -5 1

Glu Val Gly Val Ser Gly Ser Ser Ala Gly Pro Ser Thr Arg Arg Ala
5 10 15

Ala Pro Gly His Ala Ala Leu Glu Thr Gln Thr Leu Ser Ala Glu Thr 35 40 45

Ser Ser Arg Ala Ser Thr Pro Ala Gly Pro Val Pro Glu Ala Glu Thr 50 65

Arg Gly Ala Lys Arg Ile Ser Pro Ala Arg Glu Thr Arg Ser Phe Thr 70 75 80

Lys Thr Xaa Pro Asn Phe Met Val Leu Xaa Xaa Xaa Val Thr 85 90 95

(2) INFORMATION FOR SEQ ID NO: 323:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Spleen
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -21..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.9 seq WLLSDILGQGATA/NV
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

Met Gln Ser Thr Ser Asn His Leu Trp Leu Leu Ser Asp Ile Leu Gly
-20 -15 -10

Gln Gly Ala Thr Ala Asn Val Phe Arg Gly Arg His Lys Lys Thr Gly
-5 1 5 10

Asp Leu Phe Ala Ile Lys Val Phe Asn Asn Ile Ser Phe Leu Arg Pro 15 20 25

Val Asp Val Gln Met Arg Glu Phe Glu Val Leu Lys Lys Leu Asn His 30 35 40

Lys Asn Ile Val Lys Leu Phe Ala Ile Glu Glu Glu Thr Gly 45 50 55

- .1: INFORMATION FOR SEQ ID NO: 324:
 - (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 amino acids
 - (E) TYPE: AMINO ACID
 - (E) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (v1) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Lymphocytes
 - (ix) FERTURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -16..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (I) OTHER INFORMATION: score 4.9

seq ICAGSVLPPYSNC/QM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

Met Val Glu Ile Cys Ala Gly Ser Val Leu Pro Pro Tyr Ser Asn Cys
-15 -10 -5

Gln Met Pro Glu Pro Ser Ile Phe Thr Leu Ile His Phe His Thr Tyr 1 5 10 15

Tyr Cys Leu Tar Thr Pro Gln
20

- (2) INFORMATION FOR SEQ ID NO: 325:
 - (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 73 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (11' MOLECULE TYPE: PROTEIN
 - vi GRIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
 - (18) FEATURE:
 - (A) NAME/KEY: siz_peptide
 - F) LOCATION: -43..-1
 - of IDENTIFICATION METHOD: Von Heijne matrix

Met Val Ala Pro Val Leu Glu Thr Ser His Val Phe Cys Cys Pro Asn
-40 -35 . -30

Arg Val Arg Gly Val Leu Asn Trp Xaa Ser Gly Pro Arg Gly Leu Leu
-25 -20 -15

Ala Phe Gly Thr Ser Cys Ser Val Val Xaa Tyr Xaa Pro Leu Xaa Arg -10 -5 1 5

Val Val Val Thr Xaa Leu Xaa Gly His Thr Ala Arg Val Asn Cys Ile 10 15 20

Gln Trp Ile Xaa Lys Gln Xaa Gly Met 25 30

(2) INFORMATION FOR SEQ ID NO: 326:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 117 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (i1) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Lymph ganglia
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -70..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.7 seq QLLLATLQEAATT/QE
- (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly Ala
-70 -65 -60 -55

Xaa Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro Gly Glu -50 -45 -40

Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln Asp Pro Arg
-35 -30 -25

Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu Leu Ala Thr Leu
-20 -15 -10

Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala Trp Arg Lys Asn Trp
-5 1 5 10

Met Val Gly Gly Glu Gly Gly Ala Thr Gly Xaa His Arg Glu Thr Gly
15 20 25

Leu Ala Ser Val Gly Ala Gly Pro Trp Leu Gly Arg Arg Asn Pro Arg 30 35 40

Gin Leu Ser Pro **Ser**45

12' INFORMATION FOR SEQ ID NO: 327:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 91 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (V1) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Hypertrophic prostate
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -26..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.6

seq LLPFGMLCASSTT/KC

(M1) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

Met Arg Gln Thr Leu Pro Cys Ile Tyr Phe Trp Gly Gly Leu Leu Pro
-25 -20 -15

Phe Gly Met Leu Cys Ala Ser Ser Thr Thr Lys Cys Thr Val Ser His -10 5

Glu Val Ala Asp Cys Ser His Leu Lys Leu Thr Gln Val Pro Asp Asp 10 15 20

Leu Pro Thr Asn Ile Thr Val Leu Asn Leu Thr His Asn Gln Leu Arg
25 30 35

Arg Leu Pro Ala Ala Asn Phe Thr Arg Tyr Ser Gln Leu Thr Ser Leu 40 50

Asp Val Gly Phe Asn Thr Ile Ser Lys Leu Glu 55 60 65

INFORMATION FOR SEQ ID NO: 328:

- IT DEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 134 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR

- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: $-11\overline{0}..-1$
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.6

seq HTXGLLGFGRXQG/SI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

Met Ala Asp Asp Leu Glu Gln Gln Ser Gln Gly Trp Leu Ser Ser Trp
-110 -105 -100 -95

Leu Pro Thr Trp Arg Pro Thr Ser Met Ser Gln Leu Lys Asn Val Glu
-90 -85 -80

Ala Arg Ile Leu Gln Cys Leu Gln Asn Lys Phe Leu Ala Arg Tyr Val

Ser Leu Pro Asn Gln Asn Lys Ile Trp Thr Val Thr Val Ser Pro Glu
-60 -55 -50

Gln Asn Asp Arg Thr Pro Leu Val Met Val His Gly Phe Gly Gly Gly -45

Val Gly Leu Trp Ile Leu Asn Met Asp Ser Leu Xaa Ala Arg Arg Thr
-30 -25 -20 -15

Leu His Thr Xaa Gly Leu Leu Gly Phe Gly Arg Xaa Gln Gly Ser Ile
-10 -5 1

Pro Lys Gly Pro Glu Gly Leu Xaa Asp Glu Phe Val Xaa Ser Ile Xaa 5 10 15

Thr Trp Arg Glu Thr Trp 20

- (2) INFORMATION FOR SEQ ID NO: 329:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Large intestine
 - (1K) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -24..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.5 seq PLSMILLSDKIQS/SK
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

Met Lys Val Thr Gly Ile Thr Ile Leu Phe Trp Pro Leu Ser Met Ile -20 -15 -10

Leu Leu Ser Asp Lys Ile Gln Ser Ser Lys Arg Glu Val Gln Cys Asn
-5 1 5

Phe Thr Glu Lys Asn Tyr Thr Leu Ile Pro Ala Asp Ile Lys Lys Asp
10 15 20

Val Thr Ile Leu Asp Leu Ser Tyr Ash Gin Xaa Thr Leu Ash Gly Thr
25 30 35 40

Asp Thr

(2) INFORMATION FOR SEQ ID NO: 330:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (11) MOLECULE TYPE: PROTEIN
- (V1) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
- (1x) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -96..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.4

seq HLSWSSSAYQAWA/QE

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:
- Met Ala Ala Gly Arg Ala Gln Val Pro Ser Ser Glu Gln Ala Trp Leu
 -95 -85
- Glu Asp Ala Gln Val Phe Ile Gln Lys Thr Leu Cys Pro Ala Val Lys
 -80 -75 -70 -70
- Gle Pro Asn Val Gln Leu Thr Pro Leu Val Ile Asp Cys Val Lys Thr -60 -55 -50
- .a. Trp Leu Ser Gln Gly Arg Asn Gln Gly Ser Thr Leu Pro Leu Ser -45 -40 -35
- Tyr Ser Phe Val Ser Val Gln Asp Leu Lys Thr His Gln Arg Leu Pro
 -30 -25 -20
- it is to Our Bic Lou Sor Trp Sor Sor Sor Ala Ter Ole att Ter Al

(2) INFORMATION FOR SEQ ID NO: 331:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -14..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4 seq STCCWCTPGGAST/ID
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

Met Ser Thr Cys Cys Trp Cys Thr Pro Gly Gly Ala Ser Thr Ile Asp

Phe Leu Lys Arg Tyr Ala Ser Asn Thr Pro Ser Gly Glu Phe Gln Thr
5 10 15

Ala Asp Glu Asp Leu Cys Tyr Cys Leu Gly
20 25

(2) INFORMATION FOR SEQ ID NO: 332:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Cancerous prostate
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -36..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 3.9

seq VVEILPYLPCLTA/RD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

Met Pro Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile Cys Arg Asn Phe

-25

-35

Ser Asn Phe Cys Xaa Val Asp Val Val Glu Ile Leu Pro Tyr Leu Pro -20 -15 -10 -5

Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala Thr Cys Thr Leu
1 5 10

Ser Gly Asn Arg Ala

(2) INFORMATION FOR SEQ ID NO: 333:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 117 amino acids

-30

- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR
- (11) MOLECULE TYPE: PROTEIN
- (v1) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Lymph ganglia
- (1x) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -107..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 3.9

seq IVLVLLLGRYTEE/EQ

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:
- Met Ala Glu Ser Glu Asp Arg Ser Leu Arg Ile Val Leu Val Gly Lys
 -105 -100 -95
- Thr Gly Ser Gly Lys Ser Ala Thr Ala Asn Thr Ile Leu Gly Glu Glu -90 -85 -80
- Ille Phe Asp Ser Arg Ille Ala Ala Gln Ala Val Thr Lys Asn Cys Gln -75 -65 -60
- Ever Ala Ser Arg Glu Trp Gln Gly Arg Asp Leu Leu Val Val Asp Thr
 -55 -50 -45
- Fig. (Fig. 1) and the Asp Thr Lys Glu Ser Leu Xaa Thr Thr Cys Lys Glu -35 -30
- 110 Maa Arg Cys Ile Ile Ser Ser Cys Pro Gly Pro His Ala Ile Val -25 -20 -15
- Use: Val Leu Leu Gly Arg Tyr Thr Glu Glu Glu Gln Lys Thr Val -1: 5

(2) INFORMATION FOR SEQ ID NO: 334:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Lung
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -49..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 3.8

seq LLXCVGNFFGSTQ/DA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

Met Ala Gln Lys Pro Leu Arg Leu Leu Ala Cys Gly Asp Val Glu Gly
-45 -40 -35

Lys Phe Asp Ile Leu Phe Asn Arg Val Gln Ala Ile Gln Lys Xaa Ser -30 -25 -20

Gly Asn Phe Asp Leu Leu Xaa Cys Val Gly Asn Phe Phe Gly Ser Thr -15 -10 -5

Gln Asp Ala Glu Trp Glu Glu Tyr Lys Thr Gly Ile Lys Lys Ala Pro

1 5 10 15

Ile Gln Thr Tyr Val Leu Gly Ala Asn Asn Gln Glu Thr Val Lys Tyr
20 25 30

Phe Gln Asp Ala Asp Gly Cys Glu Leu Ala Glu Asn Ile Thr Tyr Leu 35 40 45

Gly Arg Gly 50

(2) INFORMATION FOR SEQ ID NO: 335:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 109 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Hypertrophic prostate
- (im) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -52..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8 seq RPVLLHLHQTAHA/DE
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:
- Met Glu Ser Arg Lys Asp Ile Thr Asn Glu Glu Glu Leu Trp Lys Met -50 -45 -40
- Lys Pro Arg Arg Asn Leu Glu Glu Asp Asp Tyr Leu His Lys Asp Thr
 -35 -30 -25
- Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His Gln
 -20 -15 -10 -5
- Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His Thr
 1 5 10
- Gln Gln Leu Phe Pro Gln Trp His Leu Pro Ile Lys Ile Ala Ala Ile 15 20 25
- He Ala Xaa Leu Thr Phe Leu Tyr Thr Leu Leu Arg Glu Val Xaa His 30 35 40
- Pro Leu Ala Thr Ser His Gln Gln Tyr Phe Tyr Lys Ile
 45 50 55
- (2) INFORMATION FOR SEQ ID NO: 336:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (v1) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Testis
 - (1x) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -52..-1
 - 10 IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 3.8

seq RPVLLHLHQTAHA/DE

- (X1) SEQUENCE DESCRIPTION: SEQ ID NO: 336:
- Net Glu Ser Arg Lys Asp Ile Thr Ash Gln Glu Glu Xaa Trp Lys Met

Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His Gln
-20 -15 -10 -5

Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His Thr

Gln Gly

(2) INFORMATION FOR SEQ ID NO: 337:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Colon
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -36..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 3.7 seq STLASVPPAATFG/AD
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:
- Met Ala Ala Thr Cys Glu Ile Ser Asn Ile Phe Ser Asn Tyr Phe Ser -35 -25
- Ala Met Tyr Ser Ser Glu Asp Ser Thr Leu Ala Ser Val Pro Pro Ala
 -20 -15 -10 -5
- Ala Thr Phe Gly Ala Asp Asp Leu Val Leu Thr Leu Ser Asn Pro Gln
 1 5 10
- Met Ser Leu Glu Gly Thr Glu Lys Ala Ser Trp Leu Gly Glu Gln Pro 15 20 25
- Gln Xaa Trp Ser Lys Thr Gln Val Leu Asp Trp Ile Ser Tyr Gln Val 30 $$\rm 35$ $\rm 40$
- Glu Lys Asn Lys Tyr Asp Ala Thr Gly 45
- (2) INFORMATION FOR SEQ ID NO: 338:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Muscle
- (1x, FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -58..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (I) OTHER INFORMATION: score 3.5

seq LVSFAVSSEGTEQ/GE

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:
- Met Arg Asp Cys Pro Gly Val Glu Xaa Ile Leu Asp Cys Ser Xaa Arg -55 -50 -45
- Gln Lys Thr Glu Gly Cys Arg Leu Gln Ala Gly Lys Glu Cys Val Asp
 -40 -35 -30
- Ser Pro Val Glu Gly Gly Gln Ser Glu Ala Pro Pro Ser Leu Val Ser -25 -20 -15
- Phe Ala Val Ser Ser Glu Gly Thr Glu Gln Gly Glu Asp Pro Arg Ser -10 -5 1 5
- Glu Lys Asp His Ser Arg Pro His Lys His Arg Ala Arg His Ala Arg 10 15 20
- Leu Arg Arg Ser Glu Ser Leu Ser Xaa Lys Gln Val Lys Glu Ala Lys
 25 30 35
- Ser Xaa Cys Lys Ser Ile Ala Leu Leu Leu Thr Asp Ala Pro Xaa Pro 40 45 50
- Ash Ser Lys Gly Val Leu Met Phe Lys Lys Arg 55 60 65
- (2) INFORMATION FOR SEQ ID NO: 339:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (11) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Cancerous prostate
 - ::x" FEATURE:
 - -A' NAME/KEY: sig_peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

Met Glu Arg Gln Ser Arg Val Met Ser Glu Lys Asp Glu Tyr Gln Phe -35 -25

Gln His Gln Gly Ala Val Glu Leu Leu Val Phe Asn Phe Leu Leu Ile
-20 -15 -10

Leu Thr Ile Leu Thr Ile Trp Leu Phe Lys Asn His Arg Phe Arg Phe -5 1 5 10

Leu His Glu Thr Gly Gly Ala Met Val Tyr
15 20

- (2) INFORMATION FOR SEQ ID NO: 340:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Cancerous prostate
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -29..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 13.4 seq SLLLVQLLTPCSA/QF
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

Met Lys Met Ala Ser Ser Leu Ala Phe Leu Leu Leu Asn Phe His Val

Ser Leu Leu Val Gln Leu Leu Thr Pro Cys Ser Ala Gln Phe Ser
-10 -5 1

Val Leu Xaa Xaa Ser Gly Pro Ile Leu Ala Met Val Gly Glu Asp Ala 5 10 15

Asp Leu 20

- (2) INFORMATION FOR SEQ ID NO: 341:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR

- (11) MOLECULE TYPE: PROTEIN
- (v1) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Normal prostate
- (1x) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -32..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 12.6

seq LLALLTVSTPSWC/QS

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:
- Met Val Phe Leu Pro Leu Lys Trp Ser Leu Ala Thr Met Ser Phe Leu
 -30 -25 -20
- Leu Ser Ser Leu Leu Ala Leu Leu Thr Val Ser Thr Pro Ser Trp Cys -15 -5
- Gln Ser Thr Glu Ala Ser Pro Lys Arg
- (2) INFORMATION FOR SEQ ID NO: 342:
 - (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Hypertrophic prostate
 - (1x) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -26..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 11.8

seq SLLLLLLXCVHWS/QP

- ERL SEQUENCE DESCRIPTION: SEQ ID NO: 342:
- Net Slu Ser Ala Ala Ala Leu His Phe Ser Arg Pro Ala Ser Leu Leu -25 -25 -15
- Ded Den Den Deu Kaa Cys Val His Trp Ser Gln Pro Ser Leu Leu Ser -1 -5 1 5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 116 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -20..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 11.2

seg AFLLLVALSYTLA/RD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

Met Glu Lys Ile Pro Val Ser Ala Phe Leu Leu Val Ala Leu Ser -20 -15 -10 -5

Tyr Thr Leu Ala Arg Asp Thr Thr Val Lys Pro Gly Ala Lys Lys Asp
1 5 10

Thr Lys Asp Ser Arg Pro Lys Leu Pro Gln Thr Leu Ser Arg Gly Trp
15 20 25

Gly Asp Gln Leu Ile Trp Thr Gln Thr Tyr Glu Glu Ala Leu Tyr Lys 30 35 40

Ser Lys Thr Ser Asn Lys Pro Leu Met Ile Ile His His Leu Asp Glu 45 50 55 60

Cys Pro His Ser Gln Ala Leu Lys Lys Val Phe Ala Glu Asn Lys Glu 65 70 75

Ile Gln Lys Leu Ala Glu Gln Phe Val Leu Leu Asn Leu Val Tyr Glu 80 85 90

Thr Thr Asp Lys

- (2) INFORMATION FOR SEQ ID NO: 344:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 amino acids
 - B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Umbilical cord

- (1x) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -46..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 10.3 seq LVLLLVLTLLCSL/VP
- (Mi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:
- Met Gly Pro Trp Gly Glu Pro Glu Leu Leu Val Trp Arg Pro Glu Ala -45 -40 -35
- Val Ala Ser Glu Pro Pro Val Pro Val Gly Leu Glu Val Lys Leu Gly
 -30 -25 -20 -15
- Ala Leu Val Leu Leu Val Leu Thr Leu Leu Cys Ser Leu Val Pro
 -10 -5 1
- Ile Cys Val Leu Arg Arg Pro Gly Ala Asn His Glu Gly Ser Ala Ser 5 10 15
- Arg Gln Lys Ala Leu Ser Pro Lys
- (2) INFORMATION FOR SEQ ID NO: 345:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 118 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (11) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Cancerous prostate
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -16..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (E) OTHER INFORMATION: score 10.1 seq LLLQLAVLGAALA/AA
 - (M1) SEQUENCE DESCRIPTION: SEQ ID NO: 345:
- Met Ala Fro Leu Leu Gl
n Leu Ala Val Leu Gly Ala Ala Leu Ala -15
 -5
- Ala Ala Ala Leu Val Leu Ile Ser Ile Val Ala Phe Thr Thr Ala Thi

Lys Gln Leu Ser Val Val Val Pro Ser Tyr Asn Glu Glu Lys Arg Leu 50 55 60

Pro Val Met Met Asp Glu Ala Leu Ser Tyr Leu Glu Lys Arg Gln Lys 65 70 75 80

Arg Asp Pro Ala Phe Thr Tyr Glu Val Ile Val Val Asp Asp Gly Ser 85 90 95

Lys Asp Gln Thr Ser Lys 100

(2) INFORMATION FOR SEQ ID NO: 346:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 127 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Lymphocytes
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -27..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 9.8 seq SALLVGFLSVIFA/LV
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

Met Ala Met Glu Gly Tyr Trp Arg Phe Leu Xaa Leu Leu Gly Ser Ala -25 -15

Leu Leu Val Gly Phe Leu Ser Val Ile Phe Ala Leu Val Trp Val Leu
-10 -5 1

His Tyr Arg Glu Gly Leu Gly Trp Asp Gly Ser Ala Leu Glu Phe Asn
10 15 20

Trp Xaa Pro Val Leu Met Val Thr Gly Phe Val Phe Ile Gln Gly Ile 25 30 35

Ala Ile Ile Val Tyr Arg Leu Pro Trp Thr Trp Lys Cys Ser Lys Leu
40 45 50

Leu Met Lys Ser Ile His Ala Xaa Leu Asn Ala Val Ala Ala Ile Leu 55 60 65

Ala Ile Ile Ser Val Val Ala Val Phe Glu Asn His Asn Val Asn Asn 70 80 85

The Ala Ash Met Tyr Ser Leu His Ser Trp Val Gly Leu Ile Ala 90 95 100

- (2) INFORMATION FOR SEQ ID NO: 347:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 129 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (11) MOLECULE TYPE: PROTEIN
 - (V1) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Lymph ganglia
 - (Ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -17..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 9.3 seq LALSLLILVLAFG/IP
 - (ML) SEQUENCE DESCRIPTION: SEQ ID NO: 347:
- Met Ala Gln Ser Leu Ala Leu Ser Leu Leu Ile Leu Val Leu Ala Phe
 -15 -10 -5
- Gly Ile Pro Arg Thr Gln Gly Ser Asp Gly Gly Ala Gln Asp Cys Cys
 1 5 10 15
- Leu Lys Tyr Ser Gln Arg Lys Ile Pro Ala Lys Val Val Arg Ser Tyr 20 25 30
- Arg Lys Gln Glu Pro Ser Leu Gly Cys Ser Ile Pro Ala Ile Leu Phe 35 40 45
- Leu Pro Arg Lys Arg Ser Gln Ala Glu Leu Cys Ala Asp Pro Lys Glu
 50 60
- Leu Trp Val Gln Gln Leu Met Gln His Leu Asp Lys Thr Pro Ser Pro 65 70 75
- Glb Lys Pro Ala Glb Gly Cys Arg Lys Asp Arg Gly Ala Ser Lys Thr
 85 90 90
- Fig. 7: by: Gly Lys Gly Ser Lys Gly Cys Lys Arg Thr Glu Arg Ser 100 105

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CO ENFORMATION FOR SEQ ID NO: 348:

- (11) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
- (1x) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -15..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 8.4

seq AMWLLCVALAVLA/WG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

Met Glu Ala Met Trp Leu Leu Cys Val Ala Leu Ala Val Leu Ala Trp -15 -5 1

Gly Phe Leu Trp Val Trp Asp Ser Ser Glu Arg Met Lys Ser Arg Glu
5 10 15

Gln Gly Xaa Arg Leu Gly Ala Glu Ser Arg Thr Leu Leu Val Ile Ala 20 25 30

His Pro Asp Asp Glu Ala Met Trp 35 40

- (2) INFORMATION FOR SEQ ID NO: 349:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
 - (ix) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -38..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 7.8

seq LVFTVSLFAWICC/QR

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:
- Val Val Gly Ile Phe Ser Ala Phe Gly Leu Val Phe Thr Val Ser Leu -20 -15 -10
- Pae Ala Trp Ile Cys Cys Gln Arg Lys Ser Ser Lys Ser Asn Lys Thr +5 1 5 10

Pro Pro Tyr Lys Phe Val His Val Leu Xaa Gly Val Asp Ile Tyr Pro
15 20 25

Glu Asn Leu Asn Ser Lys Lys Lys
30

(20 INFORMATION FOR SEQ ID NO: 350:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 121 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (11) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Umbilical cord
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -18..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 7.4 seq GWLVLCVLAISLA/SM
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:
- Met Glu Gly Pro Arg Gly Trp Leu Val Leu Cys Val Leu Ala Ile Ser
- Leu Ala Ser Met Val Thr Glu Asp Leu Cys Arg Ala Pro Asp Gly Lys
 1 5 10
- Lys Gly Glu Ala Gly Arg Pro Gly Arg Arg Gly Arg Pro Gly Leu Lys 15 20 25 30
- Gly Glu Gln Gly Glu Pro Gly Ala Pro Gly Ile Arg Thr Gly Ile Gln
 35 40 45
- Gly Leu Lys Gly Asp Gln Gly Glu Pro Gly Pro Ser Gly Asn Pro Gly 50 55 60
- Fro Gly Ile Lys Gly Thr Lys Gly Ser Pro Gly Asn Ile Lys Asp Gln

- (A) LENGTH: 79 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR -
- (11) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Muscle
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -63..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 7.2

seq VLLTLLLIAFIFL/II

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:
- Met Thr Ala Trp Glu Ala Met Ala Pro His Val Asn Pro Thr Leu Lys
 -60 -55 -50
- Asp Lys Ala Leu Ser Pro Gln Gln Xaa Xaa Xaa Thr Ser Pro Ala Pro
 -45 -40 -35
- Cys Xaa Ser Asn His His Asn Lys Lys His Leu Ile Leu Ala Phe Cys
 -30 -25 -20
- Ala Gly Val Leu Leu Thr Leu Leu Leu Ile Ala Phe Ile Phe Leu Ile
 -15 -5 1
- Ile Lys Ser Tyr Arg Lys Tyr His Ser Lys Pro Gln Ala Pro Gly
 5 10 15
- (2) INFORMATION FOR SEQ ID NO: 352:
 - (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
 - (ix) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -18..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 7.1

seq LLCECLLLXAGYA/HD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

Met Leu Cys Ser Leu Leu Leu Cys Glu Cys Leu Leu Leu Xaa Ala Gly
-15 -10 -5

Tyr Ala His Asp Asp Asp Trp Ile Asp Pro Thr Asp Met Leu Asn Tyr

1 10

Asp Ala Ala Ser Gly Thr Met Arg Lys Ser Gln Ala Lys Tyr Gly Ile 15 20 25 30

Ser Gly Glu Lys Asp Val Ser Pro Asp Leu Ser Cys Ala Xaa Glu Ile 35 40 45

Ser Glu

(2) INFORMATION FOR SEQ ID NO: 353:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (i1) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -19..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 6.9 seq LVXSLPVHCLTFA/SS
- (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 353:
- Met Gly His Ala Met Gly Leu Val Xaa Ser Leu Pro Val His Cys Leu
 -15 -10 -5
- Thr Phe Ala Ser Ser Ala Pro Ser Ser Pro Gln Pro Thr Arg Met Trp

 5 10
- The Kaa Ala Gin Ala His Xaa Pro Pro Leu Ile Leu Gly Pro 15 20 25
- I INFORMATION FOR SEQ ID NO: 354:
 - - A LENGTH: 116 amino acids
 - E TYPE: AMINO ACID

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -16..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 6.7

seq CFSLVLLLTSIWT/TR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

Met Ala Arg Cys Phe Ser Leu Val Leu Leu Leu Thr Ser Ile Trp Thr
-15 -5

Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile 1 5 10 15

Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala 20 25 30

Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu 35 40 45

Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala 50 55 60

Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val 65 70 75 80

Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly 85 90 95

Val Leu Ile Trp 100

(2) INFORMATION FOR SEQ ID NO: 355:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 65 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (1x) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -59..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 6.6

seq VLAQLAFLSQISQ/CI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

Net Leu Leu Thr Arg Lys Gln Thr Cys Gln Leu Gly Ile Leu Leu Ser
-55 -50 -45

- Ile His Arg Glr. His Ser Lys Asp Leu Gln Asp Ile Val Ala Thr Leu -40 -35 -30
- Gly Pro Arg Ser Ala Thr His Pro His Gln Pro Ala Ile Gln Val Leu
 -25 -20 -15
- Ala Gin Leu Ala Phe Leu Ser Gin Ile Ser Gin Cys Ile Ile Ser Gin
 -10 -5 1 5

Arg

- (2) INFORMATION FOR SEQ ID NO: 356:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (i1) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Cancerous prostate
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -28..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 6.6

seq IVSLLGFVATVTL/IP

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:
- Met Trp Ala Phe Ser Glu Leu Pro Met Pro Leu Leu Ile Asn Leu Ile -25 -20 -15
- Val Ser Leu Leu Gly Phe Val Ala Thr Val Thr Leu Ile Pro Ala Phe -10 -5 1
- Ary Gly His Phe Ile Ala Ala Arg Leu Cys Gly Gln Asp Leu Ash Lys 10 15 20
- Onr Ser Arg Gln Gln Ile Pro Glu Ser Gln Gly Val Ile Ser Gly Ala 25 30 35
- That Phe Leu Ile Ile Leu Phe Cys 40

- (A) LENGTH: 82 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Hypertrophic prostate
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -23..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.4

seg PASLSLLTFKVYA/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

Met Phe Lys Val Ile Gln Arg Ser Val Gly Pro Ala Ser Leu Ser Leu -20 -15 -10

Leu Thr Phe Lys Val Tyr Ala Ala Pro Lys Lys Asp Ser Pro Pro Lys
-5 5

Asn Ser Val Lys Val Asp Glu Leu Ser Leu Tyr Ser Val Pro Glu Gly
10 25

Gln Ser Lys Tyr Val Glu Glu Ala Arg Ser Gln Leu Glu Glu Ser Ile 30 35 40

Ser Gln Leu Arg His Tyr Cys Glu Pro Tyr Thr Thr Trp Cys Gln Glu
45 50 55

Thr Tyr

- (2) INFORMATION FOR SEQ ID NO: 358:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 140 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -136..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.4

seq LISVALVQGWALG/GG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

Met Ala Lys Ser Leu Leu Lys Thr Ala Ser Leu Ser Gly Arg Thr Lys -135 -125

Leu Leu His Gln Thr Gly Leu Ser Leu Tyr Ser Thr Ser His Gly Phe -120 -115 -110 -105

Tyr Glu Glu Glu Val Lys Lys Thr Leu Gln Gln Phe Pro Gly Gly Ser -100 -95 -90

The Asp Leu Gln Lys Glu Asp Asn Gly Ile Gly Ile Leu Thr Leu Asn
-85
-80
-75

Asn Pro Ser Arg Met Asn Ala Phe Ser Gly Val Met Met Leu Gln Leu -70 -65

Leu Glu Lys Val Ile Glu Leu Glu Asn Trp Thr Glu Gly Lys Gly Leu
-55 -50 -45

Ile Val Arg Gly Ala Lys Asn Thr Phe Ser Ser Gly Ser Asp Leu Asn -40 -35 -30 -25

Ala Val Lya Ser Leu Gly Leo Gln Arg Leu Pro Leu Ilo Ser Val Ala -20 -15 -10

Leu Val Gln Gly Trp Ala Leu Gly Gly Gly Ala Ala
-5

(2) INFORMATION FOR SEQ ID NO: 359:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Substantia nigra
- (1x) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (8; LGCATION: -44..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - #E] OTHER INFORMATION: score 5.3
 seq PLLKILHAAGAQG/EM
- (M1) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

Not, Tar For Pae Ser Thr Ser Ala Gln Cys Ser Thr Ser Asp Ser Ala -40 -35 -30

-10

- 5

1

Val Lys Glu Val Met His Tyr Leu Gly Gln Tyr Ile Met Val Lys Gln 5 10 15 20

- (2) INFORMATION FOR SEQ ID NO: 360:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 158 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Lung (cells)
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -112..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.1

seq AFAWLGVVPLTAC/RI

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:
- Met Asp Thr Ala Glu Glu Asp Ile Cys Arg Val Cys Arg Ser Glu Gly -110 -105 -100
- Thr Pro Glu Lys Pro Leu Tyr His Pro Cys Val Cys Thr Gly Ser Ile -95 -90 -85
- Lys Xaa Val His Gln Glu Cys Leu Val Gln Trp Leu Lys His Ser Arg
 -80 -75 -70 -65
- Lys Glu Tyr Cys Glu Leu Cys Lys His Arg Phe Ala Phe Thr Pro Ile
 -60 -55 -50
- Tyr Ser Pro Asp Met Pro Ser Arg Leu Pro Ile Gln Asp Ile Phe Ala
 -45 -40 -35
- Gly Leu Val Thr Ser Ile Gly Thr Ala Ile Arg Tyr Trp Phe His Tyr
 -30 -25 -20
- Thr Leu Val Ala Phe Ala Trp Leu Gly Val Val Pro Leu Thr Ala Cys
 -15 -5
- Arg Ile Tyr Lys Cys Leu Phe Thr Gly Ser Val Ser Ser Leu Leu Thr 1 5 10
- Leu Pro Leu Asp Met Leu Ser Thr Glu Asn Leu Leu Ala Asp Cys Leu 20 25 30
- Gln Gly Cys Phe Val Val Thr Cys Thr Leu Cys Ala Phe Ile $35 \hspace{1cm} 40 \hspace{1cm} 45$

- (2) INFORMATION FOR SEQ ID NO: 361:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (V1) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
 - (1x) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -13..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.9 seq MLIMLGIFFNVHS/AV
 - (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 361:
- Met Leu Ile Met Leu Gly Ile Phe Phe Asn Val His Ser Ala Val Leu -10 -5 1
- Ile Glu Asp Val Pro Phe Thr Glu Lys Asp Phe Glu Xaa Gly Pro Gln 5 10 15
- Asn Ile Tyr Asn Leu Tyr Glu His Gly 20 25
- (2) INFORMATION FOR SEQ ID NO: 362:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 114 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - 'vi' ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (E) TISSUE TYPE: Normal prostate
 - in, FEATURE:
 - (A, NAME/KEY: sig_peptide
 - (B) LOCATION: $-11\overline{2}..-1$
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (5) OTHER INFORMATION: score 4.5

seq AAVAVGMLXASYA/AV

CEQUENCE DESCRIPTION: SEQ ID MO. 362:

Trp Arg Trp Ile His Pro Gly Ser Pro Thr Arg Ala Ala Glu Arg Val -95 -85

Glu Pro Phe Leu Arg Pro Glu Trp Ser Gly Thr Gly Gly Ala Glu Arg
-80 -75 -70 -65

Gly Leu Arg Trp Leu Gly Thr Trp Lys Arg Cys Ser Leu Arg Ala Arg
-60 -55 -50

His Pro Ala Leu Gln Pro Pro Arg Arg Pro Lys Ser Ser Asn Pro Phe -45 -40 -35

Thr Arg Ala Xaa Glu Glu Glu Arg Arg Arg Xaa Asn Lys Thr Thr Leu
-30 -25 -20

Thr Tyr Val Ala Ala Val Ala Val Gly Met Leu Xaa Ala Ser Tyr Ala -15 -10 -5

Ala Val

(2) INFORMATION FOR SEQ ID NO: 363:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -39..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.2 seq SDPLCVLFLNTSG/QQ
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

Met Ala Ala Gln Cys Val Thr Lys Val Ala Leu Asn Val Ser Cys Ala
-35 -30 -25

Asn Leu Leu Asp Lys Asp Ile Gly Ser Lys Ser Asp Pro Leu Cys Val -20 -15 -10

Leu Phe Leu Asn Thr Ser Gly Gln Gln Trp Tyr Glu Val Glu Arg Thr
-5 5

Glu Arg Ile Lys Asn Cys Leu Asn Pro Gln Phe Ser Lys Thr Phe Ile
10 20 25

Ile Asp Tyr Tyr Phe Glu Val Val Gln Lys Leu Lys Phe Gly Val Tyr 30 35 40

Asp Ile Xaa Ash Lys Thr Ile Glu Leu Ser Asp Asp Phe Leu Gly
45 55

(1) INFORMATION FOR SEQ ID NO: 364:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (i1) MOLECULE TYPE: PROTEIN
- (v1) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (1x) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -70..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 3.7

seq AVLDCAFYDPTHA/WS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

Met Thr Gly Ser Asn Glu Phe Lys Leu Asn Gln Pro Pro Glu Asp Gly -70 -65 -60 -55

Ile Ser Ser Val Lys Phe Ser Pro Asn Thr Ser Gln Phe Leu Leu Val -50 -45 -40

Ser Ser Trp Asp Thr Ser Val Arg Leu Tyr Asp Val Pro Ala Asn Ser
-35 -30 -25

Met Arg Leu Lys Tyr Gln His Thr Gly Ala Val Leu Asp Cys Ala Phe -2C -15 -10

Tyr Asp Pro Thr His Ala Trp Ser Gly Gly Leu Asp His Xaa Xaa Lys
-5 1 5 10

Net His Asp Leu Asn Thr Asp Gln Glu Asn Leu Val Gly Thr His Asp 15 20 25

Ala Pro Ile Arg Cys Val Glu Tyr Cys Pro Ser 31

" INFORMATION FOR SEQ ID NO: 365:

: JETUENCE CHARACTERISTICS:

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -25..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 3.6

seq AHLCWCGSHCCST/CV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

Met Gly Lys His Leu Trp Tyr Pro Gly Gln Ala Ser Ala His Leu Cys -25 -15 -10

Trp Cys Gly Ser His Cys Cys Ser Thr Cys Val Phe Glu Asp Gln Leu
-5 1 5

Ser Asp Glu Arg Phe Gln Arg Ser Asn Ala Pro Ser Val Asn Ser Asp 10 15 20

- (2) INFORMATION FOR SEO ID NO: 366:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 73 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
 - (ix) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -13..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 3.5

seq MLAVSLTVXLLGA/MM

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:
- Met Leu Ala Val Ser Leu Thr Val Xaa Leu Leu Gly Ala Met Met Leu -10 -5 1
- Leu Glu Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys Glu Pro Pro 5 10 15
- Leu Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg Gln Ala Glu 20 25 30 35
- Arg Leu Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile Ala His Ile
 40 45 50

Gly Asp Val Met Phe Thr Gly Ser Trp 55 ·60

(2) INFORMATION FOR SEQ ID NO: 367:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 86 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (11) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Ovary
- (1x) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -76..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 3.5

seq MLELDLLVFHLWG/SQ

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

Met Ser Ser Thr Leu Ala Lys Ile Ala Glu Ile Glu Ala Glu Met Ala
-75 -65

Arg Thr Gln Lys Asn Lys Ala Thr Ala His His Leu Gly Leu Leu Lys -60 -55 -50 -50

Ala Arg Leu Ala Lys Leu Arg Arg Glu Leu Ile Thr Pro Lys Gly Gly -40 -35 -30

Gly Gly Gly Pro Gly Glu Gly Phe Asp Trp Pro Arg Gln Val Met -25 -15

Let. Clu Leu Asp Leu Leu Val Phe His Leu Trp Gly Ser Gln His Cys
-10 -5 1

Leu Val Thr Trp Gln Gly

1 INFORMATION FOR SEQ ID NO: 368:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 amino acids
 - (P TYPE: AMINO ACID
 - TOPOLOGY: LINEAR

- (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -45..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 13.9

seq LVLALLLVSAALS/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

Met Ala Ala Ala Val Pro Lys Arg Met Arg Gly Pro Ala Gln Ala Lys -45 -35 -30

Leu Leu Pro Gly Ser Ala Ile Gln Ala Leu Val Gly Leu Ala Arg Pro
-25 -20 -15

Leu Val Leu Ala Leu Leu Leu Val Ser Ala Ala Leu Ser Ser Val Val -10 -5 l

Ser Arg Thr Asp Ser Pro Ser Pro Leu
5 10

- (2) INFORMATION FOR SEQ ID NO: 369:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -25..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 13.9

seq LLSLLFLVQGAHG/RG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

Met Thr Pro Gln Ser Leu Leu Gln Thr Thr Leu Phe Leu Leu Ser Leu -25 -15 -10

Leu Phe Leu Val Gln Gly Ala His Gly Arg Gly His Arg Glu Asp Phe

Arg Phe Cys Ser Gln Arg Asn Gln Thr His Arg Ser Ser Leu His Tyr
10 15 20

Lys Pro Thr Pro Xaa Leu Arg Ile Ser Ile Glu Asn Ser Glu Glu 25 30 35

(2) INFORMATION FOR SEQ ID NO: 370:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 127 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (11) MOLECULE TYPE: PROTEIN
- (v1) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Testis
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -88..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 11.6 seq ILLCLLLALFASG/LI
- (M1) SEQUENCE DESCRIPTION: SEQ ID NO: 370:
- Met Met Val Val Gly Thr Gly Thr Ser Leu Ala Leu Ser Ser Leu Leu -85 -75
- Ser Leu Leu Phe Ala Gly Met Gln Ile Tyr Ser Arg Gln Leu Ala
 -70 -65 -60
- Ser Thr Glu Trp Leu Thr Ile Gln Gly Gly Leu Leu Gly Ser Gly Leu
 -55 -50 -45
- Pne Val Phe Ser Leu Thr Ala Phe Asn Asn Leu Glu Asn Leu Val Phe -40 -35 -30 -25
- Gly Lys Gly Phe Gln Ala Lys Ile Phe Pro Glu Ile Leu Leu Cys Leu
 -20 -15 -10
- Leu Leu Ala Leu Phe Ala Ser Gly Leu Ile His Xaa Val Cys Val Thr
 -5 1 5
- Thr Cys Fhe Ile Phe Ser Arg Val Gly Leu Tyr Tyr Ile Asn Lys Ile 13 20
- " INFORMATION FOR SEQ ID NO: 371:
 - : SEQUENCE CHARACTERISTICS:
 - (A: LENGTH: 134 amino acids

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Lymph ganglia
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -19..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 11.6

seq VFCLLAVAPGAHS/QE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly -15 -10 -5

Ala His Ser Gln Glu Gln Leu Val Gln Ser Gly Ala Glu Val Leu Lys $1 \hspace{1cm} 5 \hspace{1cm} 10$

Pro Gly Ala Ser Val Asn Ile Ser Cys Arg Ala Ser Gly Phe Thr Phe
15 20 25

Thr Asn Tyr Tyr Val His Trp Val Arg Gln Ala Pro Gly His Gly Leu 30 40 45

Glu Trp Met Gly Val Ile Asn Pro Val Ser Gly Tyr Thr Ser Tyr Ala
50 55 60

Gln Lys Leu Gln Gly Arg Leu Thr Met Thr Thr Asp Thr Ala Ala Asn
65 70 75

Ile Val Tyr Met Asp Leu Ser Arg Leu Lys Ser Asp Asp Thr Ala Val 80 85 90

Tyr Phe Cys Ala Lys Val Arg Cys Leu Lys Gly Ile Cys Tyr Thr Glu 95 100 105

Asp Ala Leu Asp Leu Trp 110 115

- (2) INFORMATION FOR SEQ ID NO: 372:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 139 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Umbilical cord
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: $-11\overline{3}..-1$
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 11.6

seq ILLCLLLALFASG/LI

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

Met Arg Ile Ala Asn Arg Thr Arg Phe Ser Ser Pro Phe Leu Ala Arg -110 -105 -100

Gly Ala Gly Trp Thr His Gly Arg Gly Met Met Val Val Gly Thr Gly
-95 -85

Thr Ser Leu Ala Leu Xaa Ser Leu Leu Ser Leu Leu Phe Ala Gly
-80 -75 -70

Met Gln Met Tyr Ser Arg Gln Leu Ala Ser Thr Glu Trp Leu Thr Ile
-65 -50 -55

Gln Gly Gly Leu Leu Gly Ser Gly Leu Phe Val Phe Ser Leu Thr Ala
-45 -40 -35

Phe Asn Asn Leu Glu Asn Leu Val Phe Gly Lys Gly Phe Gln Ala Lys -30 -25 -20

Fig. Pro Glu Ile Leu Leu Cys Lou Lou Leu Ala Leu Phe Ala Ser -15 -5

Gly Leu Ile His Arg Val Cys Val Thr Thr Cys Phe Ile Phe Ser Met
1 5 10 15

Val Gly Leu Tyr Tyr Ile Asn Lys Ile Ser Ser 20 25

(2) INFORMATION FOR SEQ ID NO: 373:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Heart
- ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -24.,-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 11.4 seq LMSLLLVLPWEA/VE
- x:) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

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Leu Leu Gly Val Val Leu Ser Ile Thr Gly Ile Val Pro Ala Trp 10 15 20

Gly Tyr Met His Gly

- (2) INFORMATION FOR SEQ ID NO: 374:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -20..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 11.2

seq ILVVLMGLPLAQA/LD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

Met Thr Pro Leu Leu Thr Leu Ile Leu Val Val Leu Met Gly Leu Pro -20 -15 -10 -5

Leu Ala Gin Ala Leu Asp Cys His Val Cys Xaa Tyr Asn Gly Asp Asn $1 \hspace{1cm} 5 \hspace{1cm} 10$

Cys

- (2) INFORMATION FOR SEQ ID NO: 375:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 124 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Lymph ganglia
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -16..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 11

seq LLALSLLVLWTSP/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

Met Ala Leu Leu Leu Ala Leu Ser Leu Leu Val Leu Trp Thr Ser Pro
-15 -5

Ala Pro Thr Leu Ser Gly Thr Asn Asp Ala Glu Asp Cys Cys Leu Ser 1 5 10 15

Val Thr Gln Lys Pro Ile Pro Gly Tyr Ile Val Arg Asn Phe His Tyr 20 25 30

Leu Leu Ile Lys Asp Gly Cys Arg Val Pro Ala Val Val Phe Thr Thr 35 40 45

Leu Arg Gly Arg Gln Leu Cys Ala Pro Pro Asp Gln Pro Trp Val Glu 50 55 60

Arg Ile Ile Gln Arg Leu Gln Arg Thr Ser Ala Lys Met Lys Xaa Arg 65 70 75 80

Ser Ser Xaa Pro Mct Xaa Val Xaa Arg Glu Pro Glu Ser Glu Ser Ser 85 90 95

Ile Val Asn Xaa Tyr Leu Xaa Gly Glu Arg Xaa Arg
100 105

(2) INFORMATION FOR SEQ ID NO: 376:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 103 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Umbilical cord

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -21..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 10.5 seq RLLLLPLLLAVSG/LR
 - •
- Med Gly Gly Leu Glu Pro Cys Ser Arg Leu Leu Leu Leu Pro Leu Leu -15

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1.5

20

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- Gly Asp Leu Val Leu Thr Val Leu Ile Ala Leu Ala Val Tyr Phe Leu 30 35 40
- Gly Arg Leu Val Pro Arg Gly Arg Gly Ala Ala Glu Ala Xaa Thr Arg
 45 50 55
- Lys Gln Arg Ile Thr Glu Thr Gly Ser Pro Tyr Gln Glu Leu Gln Gly 60 70 75
- Gln Arg Ser Asp Val Tyr Ser 80
- (2) INFORMATION FOR SEQ ID NO: 377:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -24..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 10 seq LCRALCLFPRVFA/AE
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:
- Met Glu Val Pro Pro Pro Ala Pro Arg Ser Phe Leu Cys Arg Ala Leu
 -20 -15 -10
- Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala Asp Ser
- Glu Val Leu Glu Glu Arg Gln Lys Arg Leu Pro Tyr Xaa Pro Glu Pro
 10 15 20
- Tyr Tyr Arg Asn Leu Asp Gly Thr Ala Ser Gly Ser Cys Xaa Ala Lys 25 30 35 40
- Met Asn Ser Arg Glu Phe Gln Arg Thr Leu Leu Ile Ser Val Arg Arg
 45 50 55

Gln Leu

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 94 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (V1) OFIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Cancerous prostate
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -19..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 9.5

seq LMCLSLCTAFALS/KP

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:
- Het Asp Leu Arg Gln Phe Leu Met Cys Leu Ser Leu Cys Thr Ala Phe
 -15 -10 -5
- Ala Leu Ser Lys Pro Thr Glu Lys Lys Asp Arg Val His His Glu Pro 1 5 10
- Gln Leu Ser Asp Lys Val His Asn Asp Ala Gln Ser Phe Xaa Tyr Asp 15 20 25
- His Asp Ala Phe Leu Gly Ala Glu Glu Ala Lys Xaa Phe Asp Gln Leu 30 40 45
- Thr Pro Glu Glu Ser Lys Glu Arg Leu Gly Lys Ile Val Ser Lys Ile
 50 55 60
- Asp Gly Asp Lys Asp Gly Phe Val Thr Val Asp Glu Leu Lys 65 70 75
- (0) INFORMATION FOR SEQ ID NO: 379:
 - (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - thi Molecule Type: PROTEIN
 - (v1) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Substantia nigra
 - ix' FFATURE:
 - A NAME/KEY: sig_peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

Met Ala Gly Gly Val Arg Pro Leu Arg Gly Leu Arg Ala Leu Cys Arg -30 -25 -20 -15

Val Leu Leu Phe Leu Ser Gln Phe Cys Ile Leu Ser Gly Gly Glu Ser
-10 -5

Thr Glu Ile Pro Pro Tyr Val Met Lys Cys Pro Ser Asn Gly Leu Cys
5 10 15

Ser Arg Leu Pro Ala Asp Cys Ile Asp Ser Thr Thr Asn Phe Ser Cys 20 25 30

Thr Tyr Gly Lys Pro Val Thr Phe Asp Cys Xaa Val Lys Pro Ser Val 35 40 45 50

Thr Cys Val Asp Gln Asp Phe Lys Ser Gln Lys Xaa Phe Ile Ile Asn
55 60 65

Met Thr Cys

- (2) INFORMATION FOR SEQ ID NO: 380:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 118 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Umbilical cord
 - (ix) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -21..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 9.3

seq VLPVILLLLGAHP/SP

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:
- Met Ala Ala Ala Trp Leu Gln Val Leu Pro Val Ile Leu Leu Leu -20 -15 -10
- Leu Gly Ala His Pro Ser Pro Leu Ser Phe Phe Ser Ala Gly Pro Ala -5 1 5 10
- Thr Val Ala Ala Ala Asp Arg Ser Lys Trp His Ile Pro Ile Pro Ser 15 20 25
- Gly Lys Asn Tyr Phe Ser Phe Gly Xaa Ile Leu Phe Arg Asn Thr Thi 30 35 40
- Ile Phe Leu Lys Phe Asp Gly Glu Pro Cys Asp Leu Ser Leu Asn Ile

45 50 55

Xaa Trp Tyr Leu Lys Ser Ala Asp Cys Tyr Asn Glu Ile Tyr Asn Phe 60 65 70 75

Lys Ala Glu Glu Val Glu Leu Tyr Leu Glu Lys Leu Lys Glu Lys Arg 80 85 90

Gly Leu Ser Gly Lys Trp
95

- (2) INFORMATION FOR SEQ ID NO: 381:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Substantia nigra
 - (1x) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -19..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 9.3 seq LLWLALACSPVHT/XL
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro
-15 -10 -5

Val His Thr Xaa Leu Ser Lys Ser Asp Ala Xaa Lys Pro Pro Arg
1 5 10

- (2) INFORMATION FOR SEQ ID NO: 382:
 - (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (11) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - TAT ORGANISM: Homo Sapiens
 - AF: TISSUE TYPE: Muscle

(3) OTHER INFORMATION: score 9.3 seq LFVAIFAVPLILG/QE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

Met Asp Val Leu Phe Val Ala Ile Phe Ala Val Pro Leu Ile Leu Gly -15 -5

Gln Glu Tyr Glu Asp Glu Glu Arg Leu Gly Glu Asp Glu Tyr Tyr Gln
1 5 10 15

Val Val Tyr Tyr Tyr Thr Val Thr Pro Ile Met Met Xaa Leu Gly Xaa 20 25 30

Xaa Phe Thr Ile Asp Tyr Xaa Ile Phe Glu Ser Glu 35

(2) INFORMATION FOR SEQ ID NO: 383:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 108 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Substantia nigra
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -21..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 9.3 seq VLPVILLLIGAHP/SP
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

Met Ala Ala Ala Trp Leu Gln Val Leu Pro Val Ile Leu Leu Leu -20 -15 -10

Leu Gly Ala His Pro Ser Pro Leu Ser Phe Phe Ser Ala Gly Pro Ala -5 1 5 10

Thr Val Ala Ala Ala Asp Arg Ser Lys Trp His Ile Pro Ile Pro Ser
15 20 25

Gly Lys Asn Tyr Phe Ser Phe Gly Lys Ile Leu Phe Arg Asn Thr Thr 30 40

Ile Phe Leu Lys Phe Asp Gly Glu Pro Cys Asp Leu Ser Leu Ash Ile 45 50 55

Thr Trp Tyr Leu Lys Ser Ala Asp Cys Tyr Ash Glu Ile Tyr Ash Phe 60 65 70 75

Lys Ala Glu Glu Val Glu Leu Tyr Leu Glu Lys Leu 80 85

- (2) INFORMATION FOR SEQ ID NO: 384:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (11) MOLECULE TYPE: PROTEIN
 - (V1) OFIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: brain
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -19..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 9.2

seq LLXLALACSPVHT/TL

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

Met Arg Thr Leu Phe Asn Leu Leu Xaa Leu Ala Leu Ala Cys Ser Pro
-15 -10 -5

Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala Ala Ser Lys

1 10

Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp Lys Pro Val Gln Asp Arg
15 20 25

Gly Leu Val Val Thr Asp Gly 30 35

- (2) INFORMATION FOR SEQ ID NO: 385:
 - (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 70 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MULECULE TYPE: PROTEIN
 - (vi) OFIGINAL SOURCE:

.

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

seq LLCLLHFSIVSVA/AX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

Met Gly Ser Lys Val Ala Asp Leu Leu Tyr Trp Lys Asp Thr Arg Thr -40 -35 -30 -25

Ser Gly Val Val Phe Thr Gly Leu Met Val Ser Leu Leu Cys Leu Leu
-20 -15 -10

His Phe Ser Ile Val Ser Val Ala Ala Xaa Phe Gly Xaa Xaa Xaa Xaa -5 5

Xaa Gly Xaa Gln Ser Ser Xaa Arg Val Tyr Ala Lys Cys Cys Arg Pro 10 15 20

Cys Thr Gly Gly Met Glu 25 30

- (2) INFORMATION FOR SEQ ID NO: 386:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Hypertrophic prostate
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -29..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 8.9 seq ALLIVCDVPSASA/QR
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val Val -25 -20 -15

Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln Arg Lys
-10 -5 i

Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met Glu Trp Thr
5 10 15

Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys Phe Arg Arg Leu 20 25 30 35

Val Lys Pro His Met

- (2) INFORMATION FOR SEQ ID NO: 387:
 - (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 137 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Umbilical cord
 - (ix) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -19..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 8.8 seq SAVLSGFVLGALA/FQ
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:
- Met Glu Gly Glu Ser Thr Ser Ala Val Leu Ser Gly Phe Val Leu Gly
 -15 -10 -5
- Ala Leu Ala Phe Gln His Leu Asn Thr Asp Ser Asp Thr Glu Gly Phe
 1 5 10
- Leu Leu Gly Glu Val Lys Gly Glu Ala Lys Asn Ser Ile Thr Asp Ser 15 20 25
- Gln Met Asp Asp Val Glu Val Val Tyr Thr Ile Asp Ile Gln Lys Tyr 30 40 45
- Ile Pro Cys Tyr Gln Leu Phe Ser Phe Tyr Asn Ser Ser Gly Glu Val
 50 55 60
- Asn Glu Gln Ala Leu Lys Lys Ile Leu Ser Asn Val Lys Lys Asn Val 65 70 75
- Val Gly Trp Tyr Lys Phe Arg Arg His Ser Asp Gln Ile Met Thr Phe 80 85 90
- Arg Glu Arg Leu Leu His Lys Asn Leu Gln Glu His Phe Ser Asn Gln 95 100 105
- Asp 100 Mal Phe Leu Leu Leu Thr Pro
- (0) INFORMATION FOR SEQ ID NO: 388:
 - : DEQUENCE CHARACTERISTICS:

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Hypertrophic prostate
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -32..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 8.8

seq VPMLLLIVGGSFG/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu -30 -25 -20

Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly Ser Phe Gly
-15 -5

Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met

1 10 15

Asp Pro Glu Arg 20

- (2) INFORMATION FOR SEO ID NO: 389:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 139 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Lymph ganglia
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: $-13\overline{6}..-1$
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 8.7

seq AVALSLFLGWLGA/DR

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:
- Met Ala Ala Trp Xaa Ser Gly Pro Ser Ala Pro Glu Ala Val Thr
 -135 -130 -125
- Ala Arg Leu Val Gly Val Leu Trp Phe Val Ser Val Thr Thr Gly Pro--120 -115 -110 -105
- Trp Gly Ala Val Ala Thr Ser Ala Gly Gly Glu Glu Ser Leu Lys Cys -100 -95 -90

Glu Asp Leu Lys Val Gly Gln Tyr Ile Cys Lys Asp Pro Lys Ile Asn
-85 -80 -75

Asp Ala Thr Gln Glu Pro Val Asn Cys Thr Asn Tyr Thr Ala His Val -70 -65 -60

Ser Cys Phe Pro Ala Pro Asn Ile Thr Cys Lys Asp Ser Ser Gly Asn -55 -50 -45

31u Thr His Phe Thr Gly Ash Glu Val Gly Phe Phe Lys Pro Ile Ser
-40 -35 -30 -25

Cys Arg Asn Val Asn Gly Tyr Ser Tyr Lys Val Ala Val Ala Leu Ser
-20 -15 -10

Leu Phe Leu Gly Trp Leu Gly Ala Asp Arg Phe
-5

- (2) INFORMATION FOR SEQ ID NO: 390:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (V1) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Normal prostate
 - (1x) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -19..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 8.6

seq LLWLALACSPVHT/TL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro

Val His Thr Thr Len Ser Lys Ser Asp Ala Lys Lys Ala Thr Ser Gly
10

- (2) INFORMATION FOR SEQ ID NO: 391:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: AMINO ACID

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -42..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 8.6

seq ASLFLLLSLTVFS/IV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

Met Asp Gly Gln Lys Lys Asn Trp Lys Asp Lys Val Val Asp Leu Leu
-40 -35 -30

Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly Ala Ser Leu
-25
-20
-15

Phe Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser Val Thr Ala -10 -5 1 5

Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser Phe Arg Ile Tyr
10 15 20

Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly His Pro Phe
25 30 35

Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser 40 45

- (2) INFORMATION FOR SEQ ID NO: 392:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 145 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Umbilical cord
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -18..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 8.5 seq LVLGLVLPLILWA/DR
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

Met Val Ala Pro Gly Leu Val Leu Gly Leu Val Leu Pro Leu Ile Leu
-15 -10 -5

Trp Ala Asp Arg Ser Ala Gly Ile Gly Phe Arg Phe Ala Ser Tyr Ile
1 5 10

Asn Asn Asp Met Val Leu Gln Lys Glu Pro Ala Gly Ala Val Ile Trp
15 20 25 30

Gly Phe Gly Thr Pro Gly Ala Thr Val Thr Val Thr Leu Arg Gln Gly 35 40 45

Gl:: Glu Thr Ile Met Lys Lys Val Thr Ser Val Lys Ala His Ser Asp
50 55 60

Thr Trp Met Val Val Leu Asp Pro Met Lys Pro Gly Gly Xaa Phe Glu 65 70 75

Val Met Ala Gln Gln Thr Leu Glu Lys Ile Asn Phe Thr Leu Arg Val 80 85 90

His Asp Val Leu Phe Gly Asp Val Trp Leu Cys Ser Gly Gln Ser Asn 95 100 105 110

Met Gln Met Thr Ala Arg Val Phe Arg Trp Arg His Val Xaa Gly Leu 115 120 125

Leu

(2) INFORMATION FOR SEQ ID NO: 393:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Ovary
- (ix) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -21..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 8.5 seq LLTIVGLILPTEG/OT
- (x1, SEQUENCE DESCRIPTION: SEQ ID NO: 393:
- Mot Gar Pro Ser Gly Arg Leu Cys Leu Leu Thr Ile Val Gly Leu Ile -20 -15 -10
- Let Pro Thr Arg Gly Gln Thr Let Lys Asp Thr Thr Ser Ser Ser Ser -9 1 5 10
- All Asy Ser Thr lie Met Asp Ile Gin Val Pro Thr Arm Ale Pro Asp

Ala Asp Glu Thr Pro Gln Pro Gln Thr Gln Thr Gln Gln Leu Glu Gly
45 50 55

Thr Asp Gly Pro Leu Val Thr Asp Pro Glu Thr Pro Arg 60 65 70

- (2) INFORMATION FOR SEQ ID NO: 394:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 114 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Prostate
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -47..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 8.3

seq LALSSLLSLLLFA/GM

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:
- Met Arg Ile Ala Asn Arg Thr Arg Phe Ser Leu Pro Phe Leu Ala Arg
 -45 -40 -35
- Gly Ala Gly Trp Thr His Gly Arg Gly Met Met Val Val Gly Thr Gly -30 -25 -20
- Thr Ser Leu Ala Leu Ser Ser Leu Leu Ser Leu Leu Leu Phe Ala Gly
 -15 -5 1
- Met Gln Met Tyr Ser Arg Gln Leu Ala Ser Thr Glu Trp Leu Thr Ile $\overline{}$ 10 $\overline{}$ 15
- Gln Gly Gly Leu Leu Gly Ser Gly Leu Phe Val Phe Ser Leu Thr Ala 20 25 30
- Phe Asn Asn Leu Glu Asn Leu Val Phe Gly Lys Gly Phe Gln Ala Lys 35 40 45

Gly Pro

- (2) INFORMATION FOR SEQ ID NO: 395:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 86 amino acids
 - (B) TYPE: AMINO ACID

- (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -35..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 8.3

seq NLLLLHCVSRSHS/QN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

Met Val Leu Gly Gly Cys Pro Val Ser Tyr Leu Leu Cys Gly Gln
-35
-20
-20

Ala Ala Leu Leu Gly Asn Leu Leu Leu His Cys Val Ser Arg
-15 -10 -5

Ser His Ser Gln Asn Ala Thr Ala Glu Pro Glu Leu Thr Ser Ala Gly
1 5 10

Ala Ala Gln Pro Glu Gly Pro Gly Gly Ala Ala Ser Trp Glu Tyr Gly
15 20 25

Asp Pro His Ser Pro Val Ile Leu Xaa Ser Tyr Leu Pro Asp Glu Phe 30 40 45

Ile Glu Cys Glu Asp Arg
50

- (2° INFORMATION FOR SEQ ID NO: 396:
 - (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (v1) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - D* DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: brain
 - (1x) FEATURE:
 - (A) NAME/KEY: sig peptide
 - B: LOCATION: -53 .-1
 - 33 IDENTIFICATION METHOD: Von Heighe matrix

Met Gly Ser Val Leu Gly Leu Cys Ser Met Ala Ser Trp Ile Pro Cys
-50 -45 -40

Leu Cys Gly Ser Ala Pro Cys Leu Leu Cys Arg Cys Cys Pro Ser Gly
-35 -30 -25

Asn Asn Ser Thr Val Thr Arg Leu Ile Tyr Ala Leu Phe Leu Leu Val-20 -15 -10

Gly Val Cys Val Ala Cys Val Met Leu Ile Pro Gly Met Glu Gln -5 5 10

Leu Asn Lys Ile Pro Gly Phe Cys Glu Asn Glu Lys Gly Val Val Pro
15 20 25

Cys Asn Ile Leu Val Gly Tyr Lys Ala Val Tyr Arg Leu Cys Phe Gly

Leu Ala Met Xaa Tyr Leu Leu Ser Leu Leu Met Ile Lys Val Lys
45 50 55

Ser Ser Ser Asp Pro Arg Ala Ala Val His Asn Gly Phe 60 65 70

(2) INFORMATION FOR SEQ ID NO: 397:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 155 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (3) LOCATION: -57..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 8

seq IVRLVAFCPFASS/OV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

Met Val Leu Leu His Val Leu Phe Glu His Ala Val Gly Tyr Ala Leu
-55 -50 -45

Leu Ala Leu Lys Glu Val Glu Glu Ile Ser Leu Leu Gln Pro Gln Val -40 +35 -30

Glu Glu Ser Val Leu Asn Leu Gly Lys Phe His Ser Ile Val Arg Leu
-25 -10 -10

Val Ala Phe Cys Pro Phe Ala Ser Ser Gln Val Ala Leu Glu Asn Ala
-5

Asn Ala Val Ser Glu Gly Val Val His Glu Asp Leu Arg Leu Leu Leu 10 15 20

Glu Thr His Leu Pro Ser Lys Lys Lys Val Leu Leu Gly Val Gly 25 30 35

Asp Pro Lys Ile Gly Ala Ala Ile Gln Glu Glu Leu Gly Tyr Asn Cys 40 45 50 55

Gin Thr Gly Gly Val Ile Ala Glu Ile Leu Arg Xaa Val Arg Leu His
60 65 70

Phe His Ash Leu Val Lys Gly Ser Asp Arg Cys Xaa Gln Leu Val Lys 75 80 85

His Ser Trp Gly Trp Asp Thr Ala Ile Pro Met 90 95

(2) INFORMATION FOR SEQ ID NO: 398:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 amino acids
 - (3) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Colon
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -47..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 7.9

seq LLLPRVLLTMASG/SP

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

Met Ser Gly Gly Arg Ala Pro Ala Val Leu Leu Gly Gly Val Ala Ser

Ten Lou Lou Ger Phe Val Trp Met Pro Ala Leu Leu Pro Val Ala Ser -3 -25 -20

Arg Leu Leu Leu Pro Arg Val Leu Leu Thr Met Ala Ser Gly Ser ~15 -5 1

Fro Pro Tor Glm Pro Ser Pro Ala Ser Asp Ser Gly Ile Gly 5 10

- (A) LENGTH: 42 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -26..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 7.8

seq LVGFILFLTRSRG/RA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

Met Val Ala Pro Val Trp Tyr Leu Val Ala Ala Ala Leu Leu Val Gly
-25 -20 -15

Phe Ile Leu Phe Leu Thr Arg Ser Arg Gly Arg Ala Ala Ser Ala Gly
-10 -5 1 5

Gln Glu Pro Leu His Asn Glu Glu Pro Gly
10 15

- (2) INFORMATION FOR SEO ID NO: 400:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -48..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 7.6

seq FLLVRKLPPLCHG/LP

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg
-45 -40 -35

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu
-30 -25 -20

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly

-15 -10 -5

Leu Pro Thr Gln Xaa Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg
1 5 10 15

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn 20 25 30

Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe 35 40 45

Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met 50 55 60

Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys
65 70 75 80

Pro Pro Leu

(2) INFORMATION FOR SEQ ID NO: 401:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 148 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Testis
- (1x) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -69..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (C) OTHER INFORMATION: score 7.6 seq FLLVRKLPPLCHG/LP
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

Met Val Gly Glu Ala Gly Arg Asp Leu Arg Arg Arg Arg Xaa Xaa Ala -65 -60 -55

Va. The Ala Waa Lys Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val +50 -40

Tyr Ser Val Pro Arg Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu
-35 -30 -25

Led Ser Ala Led Led Ser Ala Ala Phe Led Led Val Arg Lys Led Pro -20 -15 -10

Val Met Met Lys Asn Arg Arg Ser Ile Thr Val Glu Gln His Ile Ala 30 35 40

Asn Ile Phe Met Phe Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg 45 50 55

Leu Asp Ile Arg Met Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe 60 70 75

Leu Met Thr Cys

(2) INFORMATION FOR SEQ ID NO: 402:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 139 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -48..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 7.6 seq LLMLLLFLSELQY/YL
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:
- Met Glu Ala Leu Gly Lys Leu Lys Gln Phe Asp Ala Tyr Pro Lys Thr -45 -40 -35
- Leu Glu Asp Phe Arg Val Lys Thr Cys Gly Gly Ala Thr Val Thr Ile -30 -25 -20
- Val Ser Gly Leu Leu Met Leu Leu Leu Phe Leu Ser Glu Leu Gln Tyr
 -15 -5
- Tyr Leu Thr Thr Glu Val His Pro Glu Leu Tyr Val Asp Lys Ser Arg
 1 5 10 15
- Gly Asp Lys Leu Lys Ile Asn Ile Asp Val Leu Phe Pro His Met Pro 20 25 30
- Cys Ala Tyr Leu Ser Ile Asp Ala Met Asp Val Ala Gly Glu Gln Gln 35 40 45
- Leu Asp Val Glu His Asn Leu Phe Lys Gln Arg Leu Asp Lys Asp Gly 50 60
- The Pro Val Ser Ser Glu Ala Glu Arg His Glu Leu Gly Lys Val Glu 65 70 75 80

Val Thr Val Phe Asp Pro Asp Ser Leu Asp Pro 85 90

(2) INFORMATION FOR SEQ ID NO: 403:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 144 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (11) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Substantia nigra
- (1x) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -48..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 7.6
 seq FLLVRKLPPLCHG/LP
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:
- Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg
 -45 -40 -35
- Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu -30 -25 -20
- Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly -15 -5
- Leu Pro Thr Gln Arg Glu Asp Gly Asn Xaa Cys Asp Phe Asp Trp Arg

 1 10 15
- Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn 20 25 30
- Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe 35 40 45
- Jer Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ilo Arg Met
- Gly Leu Leu Xaa Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys 65 70 75 80
- Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Xaa Tyr Phe Asn Asp Lys 85 90 95

568

- (B) TYPE: AMINO ACID(D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Testis
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -19..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 7.4

seq PMLLRALAQAARA/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

Met Arg Cys Leu Thr Thr Pro Met Leu Leu Arg Ala Leu Ala Gln Ala
-15 -10 -5

Ala Arg Ala Gly Pro Pro Gly Gly Arg Ser Leu His Ser Ser Ala Val 1 5 10

Ala Ala Thr Tyr Lys Tyr Val Asn Met Gln Asp Pro Glu Met Asp Met 15 20 25

Lys Ser Val Thr Asp Arg Ala Ala Arg Thr Leu Leu Trp Thr Glu Leu 30 40 45

Phe Arg Gly Leu Gly Met Thr Leu Ser Tyr Leu Phe Arg Glu Pro Ala
50 55 60

Thr Ile Asn Tyr Pro Phe Glu Lys Gly Pro Leu Ser Pro Arg Phe Arg
65 70 75

Gly Glu His Ala Leu Arg Arg Tyr Pro Ser Gly Glu Glu Arg Cys Ile 80 85 90

Ala Cys Lys Leu Cys 95

- (2) INFORMATION FOR SEQ ID NO: 405:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
 - (ix) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -19..-1

- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.4 seq PMLLRALAQAARA/GP
- (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

Met Arg Cys Leu Thr Thr Pro Met Leu Leu Arg Ala Leu Ala Gln Ala -15 -10 -5

Ala Arg Ala Gly Pro Pro Gly Gly Arg Ser Leu His Ser Ser Ala Val $1 \hspace{1cm} 5 \hspace{1cm} 10$

Ala Ala Thr Tyr Lys Tyr Val Asn Met Gln Asp Pro Glu Met Asp Met 15 20 25

Lys Ser Val Thr Asp Arg Ala Ala Arg Thr Leu Leu Trp Thr Glu Leu 30 45

Phe Arg Gly Leu Gly Met Thr Leu Ser Tyr Leu Phe Arg Glu Pro Xaa 50 55 60

Thr Ile Asn Tyr Pro Phe Glu Lys Gly Pro Leu Ser Pro Arg Phe Arg
65 70 75

Gly Glu His Ala Leu Arg Arg Tyr Pro Ser Gly Glu Glu Arg Cys Ile 80 85 90

Ala Cys Lys Leu Cys Glu Ala Ile Cys Pro Ala Gln Ala Ile Thr Ile 95 100 105

Glu Ala Glu 110

- (2) INFORMATION FOR SEQ ID NO: 406:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 116 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (11) MOLECULE TYPE: PROTEIN
 - (V1) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYFE: Substantia nigra
 - (ix) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -21..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 7.4

seq ILPLLFGCLGVFG/LF

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys -5 5 10

Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly 15 20 25

Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu 30 35 40

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
45 50 55

Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu 60 70 75

Val Xaa Xaa Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala 80 85 90

Glu Ile Cys Ser 95

(2) INFORMATION FOR SEQ ID NO: 407:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Lymph ganglia
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -29..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 7.4 seq LLLVTWVFTPVTT/EI
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

Met His Pro Ala Val Phe Leu Ser Leu Pro Asp Leu Arg Cys Ser Leu -25

Leu Leu Val Thr Trp Val Phe Thr Pro Val Thr Thr Glu Ile Thr
-10 -5 1

Ser Leu Asp Thr Glu Xaa Ile Asp Glu Ile Leu Asn Asn Ala Leu 5 10 15

- 1) INFORMATION FOR SEQ ID NO: 408:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -20..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 7.4

seq LVFCVGLLTMAKA/ES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

Met Ala Ser Leu Gly His Ile Leu Val Phe Cys Val Gly Leu Leu Thr -20 -15 -10 -5

Met Ala Lys Ala Glu Ser Pro Lys Glu His Asp Pro Phe Thr Tyr Asp $1 \hspace{1cm} 5 \hspace{1cm} 10$

Tyr Gln Ser Leu Gln Ile Gly Gly Leu Val Ile Ala Gly Ile Leu Phe
15 20 25

Ile Leu Gly Ile Leu Ile Val Leu Ser Arg Arg Cys Arg Phe Arg 30 35 40

- (2) INFORMATION FOR SEQ ID NO: 409:
 - (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 138 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (11) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - TISSUE TYPE: Spleen
 - TEX FEATURE:
 - 'A' NAME/KEY: sig_peptide
 - B. LOCATION: -23..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - OTHER INFORMATION: score 7.3

seq ALSLLLVSGSLLP/GP

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(x1) SELUENCE DESCRIPTION: SEQ ID NO: 409:

PCT/IB98/01222

-5

5

Arg Ile Val Thr Ser Glu Glu Val Ile Ile Arg Asp Ser Pro Val Leu 10 20 25

Pro Val Thr Leu Gln Cys Asn Leu Thr Ser Ser Ser His Thr Leu Thr 30 35 40

Tyr Ser Tyr Trp Thr Lys Asn Gly Val Glu Leu Ser Ala Thr Arg Lys
45 50 55

Asn Ala Ser Asn Met Glu Tyr Arg Ile Asn Lys Pro Arg Ala Glu Asp
60 65 70

Ser Gly Glu Tyr His Cys Val Tyr His Phe Val Ser Ala Pro Lys Ala 75 80 85

Asn Ala Thr Ile Glu Val Lys Ala Ala Pro Asp Ile Thr Gly His Lys 90 95 100 105

Arg Ser Xaa Asn Lys Asn Glu Gly Gln Asp 110 115

(2) INFORMATION FOR SEQ ID NO: 410:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 amino acids
 - (3) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Lymph ganglia
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -36..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 7.2

seq IMLLSLAAFSVIS/VV

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:
- Met Ala Val His Asp Leu Ile Phe Trp Arg Asp Val Lys Lys Thr Gly
 -35
 -25
- Phe Val Phe Gly Thr Thr Leu Ile Met Leu Leu Ser Leu Ala Ala Phe -20 -15 -10 -5
- Ser Val ILe Ser Val Val Ser Tyr Leu Ile Leu Ala Leu Leu Ser Val 1 5 10
- Thr Ile Ser She Arg Ile Tyr Lys Ser Val Ile Gln Ala Val Gln Lys
 15 20 25
- Ser Glu Glu Giy His Pro Phe Lys Ala Tyr Leu Asp Val Asp Ile Thr

40

30

Leu Ser Ser Glu Ala Phe His Asn Tyr Met Asn Ala Ala Met Val His

(2) INFORMATION FOR SEQ ID NO: 411:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 amino acids

35

- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (v1) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Lymph ganglia
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -32..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (E) OTHER INFORMATION: score 7.1

seq LLWTLLLFAAPFG/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

Met Xaa Gly Ser Val Glu Cys Thr Xaa Gly Trp Gly His Cys Ala Pro
-30 -25 -20

Ser Pro Leu Leu Trp Thr Leu Leu Phe Ala Ala Pro Phe Gly
-15 -10 -5

Leu Leu Gly Glu Lys Thr Arg Gln Val Ser Leu Glu Val Ile Pro Asn
1 5 10 15

Trp Leu Gly Pro Leu Gln Asn Leu Leu His Ile Arg Ala Val Gly Thr
20 25 30

Asn Ser Thr Leu His Tyr Val Trp Ser Ser Leu Gly Pro Leu Ala Val 35 40 45

Val Met Val Ala Thr Asn Thr Pro Pro Gly 50 55

- I INFORMATION FOR SEQ ID NO: 412:
 - (1) JEQUENCE CHARACTERISTICS:
 - TA TENGTH: 97 amino acids

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- TYPE: AMINO ACID
- TOPOLOGY: LINEAR

(F) TISSUE TYPE: Normal prostate

- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (E) LOCATION: -29..-1
 - (3) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 7.1

seq LIFLCGAALLAVG/IW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu -25 -20 -15

Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val

Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser 5 10 15

Ser Ala Met Gin Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly 20 25 30 35

Val Val Phe Ala Leu Gly Phe Leu Gly Cys Xaa Gly Ala Lys Xaa 40 45 50

Glu Xaa Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Ile 55 60 65

Phe

- (2) INFORMATION FOR SEQ ID NO: 413:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 120 amino acids
 - (E) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Testis
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -32..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 7.1

seq LLWTLLLFAAPFG/LL

(M1) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

Met Arg Gly Ser Val Glu Cys Thr Trp Gly Xaa Gly His Cys Ala Pro

Ser Pro Len Leu Eu Trp Thr Leu Leu Phe Ala Ala Pro Phe Gly

-15 -10 -5

Leu Leu Gly Glu Lys Thr His Gln Val Ser Leu Glu Val Ile Pro Asn
1 5 10 15

Trp Leu Gly Pro Leu Gln Asn Leu Leu His Ile Arg Xaa Val Gly Thr 20 25 30

Asn Ser Thr Leu His Tyr Val Trp Ser Ser Leu Gly Pro Leu Ala Val 35 40 45

Val Met Val Ala Thr Asn Thr Pro His Ser Thr Leu Ser Val Asn Trp 50 55 60

Ser Leu Leu Ser Pro Glu Pro Asp Gly Gly Leu Met Val Leu Pro 65 70 75 80

Lys Asp Ser Ile Gln Phe Ser Ser 85

(2) INFORMATION FOR SEQ ID NO: 414:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Lymphocytes
- (1%) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -15..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 7

seq LRLLKLAATSASA/RV

(wil) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

Not Al. 100 Arg Leu Leu Lys Leu Ala Ala Thr Ser Ala Ser Ala Arg -15 -5 1

 $74.\ 7.5\ \mathrm{Arg}$ Ala Gly Ala Gln Arg Val Arg Gly Ile His Ser Ser Val -5

Gin Cys bys Leu Arg Tyr Gly Met Trp His Phe Leu Leu Gly Asp Lys

Alsoling to Arg Leu Thr Glu Arg Ser Arg Val Ile Thr Val Asp Gly
40 45

- (2) INFORMATION FOR SEQ ID NO: 415:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 116 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Cancerous prostate
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -65..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 7

seq IGHFLCLVILVYC/AE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

Met Pro Ser Ala Phe Ser Val Ser Ser Phe Pro Val Ser Ile Pro Ala -65 -50 -50

Val Leu Thr Gln Thr Asp Trp Thr Glu Pro Trp Leu Met Gly Leu Ala-45 -40 -35

Thr Phe His Ala Leu Cys Val Leu Leu Thr Cys Leu Ser Ser Arg Ser
-30 -25 -20

Tyr Arg Leu Gln Ile Gly His Phe Leu Cys Leu Val Ile Leu Val Tyr
-15 -10 -5

Cys Ala Glu Tyr Ile Asn Glu Ala Ala Ala Met Asn Trp Arg Leu Phe
1 5 10 15

Ser Lys Tyr Gln Tyr Phe Asp Ser Arg Gly Met Phe Ile Ser Ile Val 20 25 30

Phe Ser Ala Pro Leu Leu Val Asn Ala Met Ile Ile Val Val Met Trp 35 40 45

Val Trp Lys Thr 50

- (2) INFORMATION FOR SEQ ID NO: 416:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 163 amino acids
 - (B) TYPE: AMINO ACID
 - [D] TOPOLOGY: LINEAR
 - (11) MOLECULE TYPE: PROTEIN
 - (V.) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Testis

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) L@CATION: -154..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6.7

seq ALGILVVAGCSFA/IR

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

Met Ala Leu Pro His Gl
n Glu Pro Lys Pro Gly Asp Leu Ile Glu Ile -150
 -145
 -140

Phe Arg Leu Gly Tyr Glu His Trp Ala Leu Tyr Ile Xaa Asp Gly Tyr
-135
-125

Val Ile His Leu Ala Pro Pro Ser Glu Tyr Pro Gly Ala Gly Ser Ser -120 -115 -110

Ser Val Phe Ser Val Leu Ser Asn Ser Ala Glu Val Lys Arg Glu Arg
-105 -100 -95

Leu Glu Asp Val Val Gly Gly Cys Cys Tyr Arg Val Asn Asn Ser Leu -90 -85 -80 -75

Asp His Glu Tyr Gln Pro Arg Pro Val Glu Val Ile Ile Ser Ser Ala
-70 -65 -60

Lys Glu Met Val Gly Gln Lys Met Lys Tyr Ser Ile Val Ser Arg Asn
-55 -50 -45

Cys Glu His Phe Val Thr Gln Leu Arg Tyr Gly Lys Ser Arg Cys Lys
-40 -35 -30

Gin Val Glu Lys Ala Lys Val Glu Val Gly Val Ala Thr Ala Leu Gly
-25 -20 -15

Lys Ala Thr

1 INFORMATION FOR SEQ ID NO: 417:

. JEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

11 MOLECULE TYPE: PROTEIN

. DFIGINAL SOURCE:

- (B) LOCATION: -70..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7 seg LAFSLPALPLAEL/OP

(M1) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

Met Ala Ala Ser Thr Ser Met Val Pro Val Ala Val Thr Ala Ala Val -70 -65 -60 -55

Ala Pro Val Leu Ser Ile Asn Ser Asp Phe Ser Asp Leu Arg Glu Ile
-50 -45 -40

Lys Lys Gln Leu Leu Leu Ile Ala Gly Leu Thr Arg Glu Arg Gly Leu -35 -30 -25

Leu His Ser Ser Lys Trp Ser Ala Glu Leu Ala Phe Ser Leu Pro Ala -20 -15 -10

Leu Pro Leu Ala Glu Leu Gln Pro Pro Pro Pro Ile Thr Glu Glu Asp
-5 1 5 10

Ala Gln Asp Met Asp Ala Tyr Thr Leu Ala Lys Ala Tyr Phe Asp Val\$15\$ 20 \$25\$

Lys Glu Tyr Asp Arg Ala Ala His Phe Leu His Gly Cys Asn Ala Arg 30 35 40

Xaa Ala Tyr Phe Leu Tyr Met Tyr Ser Arg Tyr Leu Ser 45 50 55

(2) INFORMATION FOR SEQ ID NO: 418:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 94 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (11) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Hypertrophic prostate
- (1x) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -24..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 6.6 seq KMVHLLVLSGAWG/MQ
- inii SEQUENCE DESCRIPTION: SEQ ID NO: 418:

Met 3.4 Glu Gly Gly Asn Leu Gly Gly Leu Ile Lys Met Val His Leu -20 -15 -10

Let Wel Let Ser Gly Ala Trp Gly Met Gln Met Trp Val Thr Phe Val

- 5

1

Ser Gly Pne Leu Leu Phe Arg Ser Leu Pro Arg His Thr Phe Gly Leu 10 20

Val Gln Ser Lys Leu Phe Pro Phe Tyr Phe His Ile Ser Met Gly Cys
25 30 35 40

Ala Phe Ile Asn Xaa Cys Ile Leu Ala Ser Gln His Ala Trp Ala Gln 45 50 55

Leu Thr Phe Trp Glu Ala Ser Gln Leu Tyr Leu Leu Phe Leu 60 65 70

(2) INFORMATION FOR SEQ ID NO: 419:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (V1) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (1x) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -81..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 6.6 seq LLLASGTTLFCTS/FY
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:
- Met Ala Gly Pro Ala Ala Ala Phe Arg Arg Leu Gly Ala Leu Ser Gly -80 -75 -70
- Ala Ala Leu Gly Phe Ala Ser Tyr Gly Ala His Gly Ala Xaa Phe
 -8: -55 -50
- r: Asp Ala Tyr Gly Lys Glu Leu Phe Asp Lys Ala Asn Lys His His -45 -40 -35
- 1890 His Ser Leu Ala Leu Leu Gly Val Pro His Cys Arg Lys Pro -30 -25 -20
- U . 1rp Ala Gly Leu Leu Leu Ala Ser Gly Thr Thr Leu Phe Cys Thr
 -15 -10 -5

- - Tyr Tyr Sln Ala Gln

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (i1) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Testis
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -21..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 6.5

seq LLTLLLPPPPPLYT/RH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

Met Gly His Arg Phe Leu Arg Gly Leu Leu Thr Leu Leu Pro Pro -20 -15 -10

Pro Pro Leu Tyr Thr Arg His Arg Met Leu Gly Pro Glu Ser Val Pro -5 1 5 10

Pro Pro Lys Arg Ser Arg Ser Lys Leu Met Ala Pro Pro Arg 15 20 25

- (2) INFORMATION FOR SEQ ID NO: 421:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -20..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 6.5

seq ILFLLPSICSSNS/TG

(Mi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

Mac Stu Leu Leu Gln Val Thr Ile Leu Phe Leu Leu Pro Ser Ile Cys -15 -10 -5

Jer Ser Ash Ser Thr Gly Val Leu Glu Ala Ala Ash Ash Ser Leu Val

10

Val Thr Thr Thr Xaa Pro Ser Ile Thr Thr Pro Asn Thr Glu Ser Leu 15 20 25

Gln Lys Asn Val Val Thr Pro Thr Thr Gly Thr Thr Xaa Lys Gly Thr 30 40

Ile Thr Ash Glu Leu Leu Lys Met Ser Leu Met Ser Thr Ala Xaa Phe
45
50
55
60

(2) INFORMATION FOR SEQ ID NO: 422:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 117 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (11) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Lung (cells)
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -19..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 6.3 seq VLMRLVASAYSIA/QK
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:
- Met Ala Ser Ser Asn Thr Val Leu Met Arg Leu Val Ala Ser Ala Tyr
 -15 -10 -5
- Ser He Ala Gln Lys Ala Gly Met He Val Arg Arg Val He Ala Glu 1 5 10
- Gly Asp Leu Gly Ile Val Glu Lys Thr Cys Ala Thr Asp Leu Gln Thr
 15 20 25
- Lys Ala Asp Arg Leu Ala Gln Met Ser Ile Cys Ser Ser Leu Ala Arg
- ing fro Lys Leu Thr Ile Ile Gly Glu Glu Asp Leu Pro Ser Glu
 50 55 60
- Fig. Val. Asp Gln Glu Leu Ile Glu Asp Ser Gln Trp Glu Glu Ile Leu 65 70 75
 - In the Cyc Pro Ser Glm Tyr Ser Ala Ile Lys Glu Glu Asp Leu 85 90

- (2) INFORMATION FOR SEQ ID NO: 423:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 117 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -15..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 6.3

seq SSCVLLTALVALA/AY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

Met Arg Ser Ser Cys Val Leu Leu Thr Ala Leu Val Ala Leu Ala Ala -15 -5 1

Tyr Tyr Val Tyr Ile Pro Leu Pro Gly Ser Val Ser Asp Pro Trp Lys
5 10 15

Leu Met Leu Leu Asp Ala Thr Phe Arg Gly Ala Gln Gln Val Ser Asn 20 25 30

Leu Ile His Tyr Leu Gly Leu Ser His His Leu Leu Ala Leu Asn Phe 35 40 45

The The Val Ser Phe Gly Lys Lys Ser Ala Trp Ser Ser Ala Gln Val
50 65

Lys Val Thr Asp Thr Asp Phe Asp Gly Val Glu Val Arg Val Phe Glu
70 75 80

Gly Pro Pro Lys Pro Glu Glu Pro Leu Lys Arg Ser Val Val Tyr Ile
85 90 95

His Gly Xaa Gly Trp 100

- (2) INFORMATION FOR SEQ ID NO: 424:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 74 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (i1) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens

- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3 seq GVGLVTLLGLAVG/SY
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:
- Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly
 -25
 -20
 -15
- Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg -10 -5 1 5
- Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Asn Glu Lys Tyr Leu 10 15 20
- Lou Arg Leu Leu Asp Lys Thr Thr Val Ser His Asn Thr Lys Arg Phe
 25 30 35
- Arg Phe Ala Leu Pro Thr Ala His His Met 40 45

(2) INFORMATION FOR SEQ ID NO: 425:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 88 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) OFIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: brain
- (ix) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -69..-1
 - (3) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 6.3

seq ILLIVLFLDAVRE/VR

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

The During Sln Trp Ala Ala Val Ala Thr Phe Leu Tyr Ala Glu Ile -65 -60 -55 **-**35

-30

-25

Asn Lys Ala Phe Leu Thr Ile Ile Ile Leu Leu Ile Val Leu Phe Leu -20 -15 -10

Asp Ala Val Arg Glu Val Arg Lys Tyr Ser Ser Val His Thr Ile Glu
-5 1 5 10

Lys Ser Ser Thr Ser Arg Pro Arg

(2) INFORMATION FOR SEQ ID NO: 426:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 94 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -85..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 6.2 seq FLDFCVYIPLSWG/FC
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

Met Pro Ser Glu Gly Arg Cys Trp Glu Thr Leu Lys Ala Leu Arg Ser
-85 -75 -70

Ser Asp Lys Gly Arg Leu Cys Tyr Tyr Arg Asp Trp Leu Leu Arg Arg
-65 -60 -55

Slu Val Ser Gly Gly Pro Gly Gly Arg Arg Pro Phe Arg Pro Leu Ala
-50 -45 -40

Thr Glu Thr Phe Ser Leu Ala Val Gly Thr Phe Cys Ser Arg Glu Pro
-35 -25

Val Gin Ser Asn Asn Leu His Leu Phe Leu Asp Phe Cys Val Tyr Ile
-20 -15 -10

Fro Leu Ser Trp Gly Phe Cys Pro Leu Gln Pro Ile Leu Ala

- INFOPMATION FOR SEQ ID NO: 427:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids

- (B) TYPE: AMINO ACID (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Umbilical cord
- (1x) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -24..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (0) OTHER INFORMATION: score 6.2

seq AILGSTWVALTTG/AL

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

Met Thr Lys Leu Ala Gln Trp Leu Trp Gly Leu Ala Ile Leu Gly Ser -20 -15

Thr Trp Val Ala Leu Thr Thr Gly Ala Leu Gly Leu Glu Leu Pro Leu

Ser Cys Gin Giu Val Leu Trp Pro Leu Pro Ala Tyr Leu Leu Val Ser 15

Ala Gly Cys Tyr Ala Leu Gly Thr Val Gly Tyr Arg Val Ala Thr Phe

His Asp Cys Slu Asp Ala Ala Arg Glu Leu Gln Ser Gln Ile Gln Glu

Ala Arg Ala Asp Leu Ala Arg Xaa Gly Cys Ala Ser Asp Ser Leu Xaa 60 70

Pro Phe Leu Cys Gly Gln Pro Phe Leu Pro Phe Pro Ile Lys Glu Pro

317

- (2) INFORMATION FOR SEQ ID NO: 428:
 - (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

- (B) TYPE: AMINO ACID
 (C) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) CEGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Normal prostate

- (D) OTHER INFORMATION: score 6.2 seq FLVSNMLLAEAYG/SG
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

Met Leu Leu Ala Trp Val Gl
n Ala Phe Leu Val Ser As
n Met Leu Leu -20 -15 -10

Ala Glu Ala Tyr Gly Ser Gly Gly Cys Phe Trp Asp Asn Gly His Leu
-5 1 5 10

Tyr Arg Glu Asp Gln Thr Ser Pro Ala Pro Gly Leu Arg Cys Leu Asn 15 20 25

Trp Leu Asp Ala Gln Ser Gly 30

- (2) INFORMATION FOR SEQ ID NO: 429:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -41..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 6.2 seq SVLVLLLLAVLYE/GI
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

Met Ala Met His Phe Ile Phe Ser Asp Thr Ala Val Leu Leu Phe His

Phe Trp Ser Val His Ser Pro Ala Gly Met Ala Leu Ser Val Leu Val -25 -10

Leu Leu Leu Ala Val Leu Tyr Glu Gly Ile Lys Val Gly Lys Ala
-5 1 5

Lys Leu Asn Gln Val Leu Val Asn Leu Pro Thr Ser Ile Ser Gln
10 15 20

Oln Thr Ile Ala Glu Thr Asp Gly Asp Ser Ala Gly Ser Asp Ser Phe 25 30 35

Pro Val Gly Arg Thr His His Arg Trp Tyr Leu Cys His Phe Gly Gln 55

Ser Leu Ile His Val Ile Gln Val Val Ile Gly Tyr Phe Ile Met Leu 60 65 70

Ala Val Met Ser Tyr Asn Thr Trp Ile Phe Leu Gly Val Val 75 80 85

... INFORMATION FOR SEQ ID NO: 430:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (V1) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -75..-1
 - (2) IDENTIFICATION METHOD: Von Heijne matrix
 - (C) OTHER INFORMATION: score 6.2 seq VVXXSVLXTTCXS/SQ
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

Met Lys Gln Val His Gln Cys Ile Glu Arg Cys His Val Pro Leu Ala -75 -65 -60

Gin Ala Gin Ala Leu Val Thr Ser Glu Leu Glu Lys Phe Gin Asp Arg -55 -50 -45

Led Ala Arg Cys Thr Met His Cys Asn Asp Lys Ala Lys Asp Ser Ile
-40 +35 -30

Asp Ala Gly Xaa Lys Glu Leu Gln Val Lys Gln Gln Leu Xaa Val Val -25 -20 -15

Ada Xaa Ser Val Leu Xaa Thr Thr Cys Xaa Ser Ser Gln Leu -10 -5 1

INFURMATION FOR SEQ ID NO: 431:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - 1: MOLECULE TYPE: PROTEIN

- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -27..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 6.2 seq LLAALMLVAMLQL/LY
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

Met Gln Met Ser Tyr Ala Ile Arg Cys Ala Phe Tyr Gln Leu Leu Leu -25 -15

Ala Ala Leu Met Leu Val Ala Met Leu Gln Leu Leu Tyr Leu Ser Leu
-10 -5 1 5

Leu Ser Gly Leu His Gly Pro
10

- (2) INFORMATION FOR SEQ ID NO: 432:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Umbilical cord
 - (ix) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (3) LOCATION: -19..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 6.1

seg IILLIHTMOVCTT/HP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

Met Met Thr Gln Thr Cys Ile Ile Leu Leu Ile His Thr Met Gln Val-15 -10 -5

Cys Thr Thr His Pro Thr Val Leu Ser His Thr Leu Leu Gln Arg Pro 1 5 10

Lys Pro Thr Asp Leu Phe Pro Lys Ala Thr Pro Thr Thr Ala Pro Met
15 20 25

Pro Leu Arg Met Arg Pro Pro Gln Cys Leu Pro Glu 30 40

- (2) INFORMATION FOR SEQ ID NO: 433:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (v1) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (1x) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -22..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 6.1

seg LFLTCLFWPLAAL/NV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

Met Xaa Xaa His Leu Gln Thr Arg Pro Leu Phe Leu Thr Cys Leu Phe -20 -15 -10

Trp Pro Leu Ala Ala Leu Asn Val Asn Ser Thr Phe Glu Cys Leu Ile
-5 1 5 10

Leu Gln Cys Ser Val Gly Ile 15

- (2) INFORMATION FOR SEQ ID NO: 434:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 92 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Testis
 - .ix' FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -52..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 6.1

seq LMAFLLSFYLIFT/NE

- (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 434:
- The Fire Nic Ash Tyr Ser Ser Thr Xaa Thr Arg Arg Glu His Val Lys

Ser Gly Gly Met Phe Val Gly Leu Met Ala Phe Leu Leu Ser Phe Tyr-20 -15 -10 -5

Leu Ile Phe Thr Asn Glu Gly Arg Ala Leu Lys Thr Ala Thr Ser Leu $1 \hspace{1cm} 5 \hspace{1cm} 10$

Ala Glu Gly Leu Ser Leu Val Val Ser Pro Asp Ser Ile His Ser Val

Ala Pro Glu Asn Glu Gly Xaa Leu Val His Ile Ile 30 35 40

- (2) INFORMATION FOR SEQ ID NO: 435:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Cancerous prostate
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -21..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 6.1

seq LEMLTAFASHIRA/RD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

Met Arg Gly Ala His Leu Thr Ala Leu Glu Met Leu Thr Ala Phe Ala -20 -15 -10

Ser His Ile Arg Ala Arg Asp Ala Ser Gly
-5 1 5

- (2) INFORMATION FOR SEO ID NO: 436:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Cancerous prostate
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -24..-1

- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1 seq IILLIHTMQVCTT/HP
- (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

Met Val His Lys Pro Met Met Thr Gln Thr Cys Ile Ile Leu Leu Ile -20 -15 -10

His Thr Met Gln Val Cys Thr Thr His Pro Thr Val Leu Ser His Thr -5 1 5

Leu Leu Gln Arg Pro Lys Pro Thr Asp Leu Phe Pro Lys Ala Thr Pro
10 20

Thr Thr 25

- (2) INFORMATION FOR SEQ ID NO: 437:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Cancerous prostate
 - (ix) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -28..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 6 seq IGLMFLMLGCALP/IY
 - (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

Mor Ala Gly Ile Lys Ala Leu Ile Ser Leu Ser Phe Gly Gly Ala Ile
-25 -20 -15

1., Let Phé Léu Met Leu Gly Cys Ala Leu Pro Ile Tyr Ash Lys -10 -5 1

The Trp Pro Thr

. INFORMATION FOR SEQ ID NO: 438:

- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -21..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 6

seq LLFPLTLVRSFWS/DM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

Met Ser Leu Met Pro Lys Met His Leu Leu Phe Pro Leu Thr Leu Val

Arg Ser Phe Trp Ser Asp Met Met Asp Ser Ala Gln Ser Phe Ile Thr -5 1 5 10

Ser Ser Trp Thr Phe Tyr Leu Gln Ala Asp Asp Gly Lys Ile Val Ile
15 20 25

Phe Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro His Leu Glu Gln Glu 30 35 40

Pro Thr Asn Leu Arg Glu Ser Ser Leu Ser Lys Met Ser Tyr Leu Gln
45 50 55

Met Arg Asn Ser Gln Ala His Arg 60 65

- (2) INFORMATION FOR SEQ ID NO: 439:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 115 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Lung
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -87..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.9 seq SNILLASVGSVLG/AC
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

-85

-75

-80

Gly Ala Val Pro Val Val Leu Ser Ala Met Gly Phe Thr Gly Ala Gly
-70 -65 -60

Ile Ala Ala Ser Ser Ile Ala Ala Lys Met Met Ser Ala Ala Ile
-55 -45 -40

Ala Asn Gly Gly Val Ser Ala Gly Ser Leu Val Ala Thr Leu Gln -35 -30 -25

Ser Vai Gly Ala Ala Gly Leu Ser Thr Ser Ser Asn Ile Leu Leu Ala
-20 -15 -10

Ser Val Gly Ser Val Leu Gly Ala Cys Leu Gly Asn Ser Pro Ser Xaa -5 5

Ser Leu Pro Ala Glu Pro Xaa Xaa Xaa Glu Asp Glu Ala Arg Glu Asn 10 20 25

Val Pro Pro

(2) INFORMATION FOR SEQ ID NO: 440:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -14..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.8

seq VTIILLLSCXFWA/VK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

Max Val Thr Ile Ile Leu Leu Leu Ser Cys Xaa Phe Trp Ala Val Lys
-10 -5 1

Asn Val Thr Xaa Arg Xaa Met Val Gly Leu Arg Trp Trp Asn His Ile 5 10 15

. INFORMATION FOR SEQ ID NO: 441:

- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Lung
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -87..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.8

seq SNILLASVGSVSG/AC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

Met Xaa Lys Arg Ala Ala Ala Ala Ala Val Gly Gly Ala Leu Ala Val -85 -80 -75

Gly Ala Val Pro Val Val Leu Ser Ala Met Gly Phe Thr Gly Ala Gly -70 -65 -60

Ile Ala Ala Ser Ser Ile Ala Ala Lys Met Met Ser Ala Ala Ile
-55 -45 -40

Ala Asn Gly Gly Val Ser Ala Gly Ser Leu Val Ala Thr Leu Gln
-35 -30 -25

Ser Val Gly Ala Ala Gly Leu Ser Thr Ser Ser Asn Ile Leu Leu Ala
-20 -15 -10

Ser Val Gly Ser Val Ser Gly Ala Cys Leu Gly Asn Ser Pro Ser Ser -5

Ser Leu Pro Ala Glu Pro Glu Ala Lys Glu Asp Glu Ala Arg Glu Asn 10 20 25

Val Pro Gln Gly Glu Pro Pro Lys Pro Pro Leu Lys Ser Glu Lys His 30 35 40

Glu Arg

(2) INFORMATION FOR SEQ ID NO: 442:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 118 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -89..-1

- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7 seq DLSLLSLPPGTSP/VG
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

Met Ser Gln Asp Gly Gly Xaa Gly Glu Leu Lys His Met Val Met Ser
-85 -80 -75

Pne Arg Val Ser Glu Leu Gln Val Leu Leu Gly Xaa Xaa Gly Arg Asn -70 -65 -60

Lys Ser Gly Arg Lys His Glu Leu Leu Ala Lys Ala Leu His Leu Leu -55 -45

Lys Ser Ser Cys Ala Pro Ser Val Gln Met Lys Ile Lys Glu Leu Tyr
-40 -35 -30

Arg Arg Arg Phe Pro Arg Lys Thr Leu Gly Pro Ser Asp Leu Ser Leu -25 -15 -10

Leu Ser Leu Pro Pro Gly Thr Ser Pro Val Gly Ser Pro Gly Pro Leu
-5 5

Ala Pro Ile Pro Pro Thr Xaa Leu Ala Xaa Ala Xaa Cys Trp Ala Pro
10 15 20

Ser Val Arg Trp Thr Cys 25

(2) INFORMATION FOR SEO ID NO: 443:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Spleen
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -24..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.7

seq LLLPRVLLTMASG/SL

(M1) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

Pro Arg Ile Pro Xaa Leu Ala Thr Phe Arg Xaa Arg Ser Leu 10 15 20

(2) INFORMATION FOR SEQ ID NO: 444:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 122 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -35..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.7 seq IFSFLDIVTLCRC/AQ
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

Met Val Phe Ser Asn Asn Asp Glu Gly Leu Ile Asn Lys Lys Leu Pro
-35 -25 -20

Lys Glu Leu Leu Arg Ile Phe Ser Phe Leu Asp Ile Val Thr Leu
-15 -10 -5

Cys Arg Cys Ala Gln Ile Xaa Lys Ala Trp Asn Ile Leu Ala Leu Asp 1 5 10

Gly Ser Asn Trp Gln Arg Ile Asp Leu Phe Asn Phe Gln Thr Asp Val 15 20 25

Glu Gly Arg Val Val Glu Asn Ile Ser Lys Arg Cys Gly Gly Phe Leu 30 45

Arg Lys Leu Ser Leu Arg Gly Cys Ile Gly Val Gly Xaa Ser Ser Leu 50 55 60

Xaa Thr Phe Ala Gln Asn Cys Arg Asn Ile Glu His Leu Asn Leu Asn 65 70 75

Gly Cys Thr Lys Ile Thr Xaa Ser Thr Cys 80 85

(2) INFORMATION FOR SEQ ID NO: 445:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 amino acids
 - (B) TYPE: AMINO ACID

- (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (v1) ORIGIMAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
- (ix) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -35..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.7

seq IFSFLDIVTLCRC/AQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

Met Val Phe Ser Asn Asn Asp Glu Gly Leu Ile Asn Lys Lys Leu Pro -35 -25 -20

Lys Glu Leu Leu Leu Arg Ile Phe Ser Phe Leu Asp Ile Val Thr Leu
-15 -10 -5

Cys Arg Cys Ala Gln Ile Ser Lys Ala Trp Asn Ile Leu Ala Leu Asp 1 5 10

Gly Ser Asn Trp Gln Gly
15

- (2) INFORMATION FOR SEQ ID NO: 446:
 - (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 145 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Umbilical cord
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (F) LOCATION: -112..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (2) (THER INFORMATION: score 5.6

seq SSCILPWLSKTNS/CP

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:
- Not Alla Ger Tur Phe Asp Glu His Asp Cys Glu Pic Ser Asp Pro Tel

Asn Arg Met Asp Phe Glu Asp Leu Gly Leu Val Val Asp Trp Asp His -80 -75 -70 -65

His Leu Pro Pro Pro Ala Ala Lys Thr Val Val Glu Asn Leu Pro Arg
-60 -55 -50

Thr Val Ile Arg Gly Ser Gln Ala Glu Leu Lys Cys Pro Val Cys Leu
-45 -40 -35

Leu Glu Phe Glu Glu Glu Glu Thr Ala Ile Glu Met Pro Cys His His
-30 -25 -20

Leu Phe His Ser Ser Cys Ile Leu Pro Trp Leu Ser Lys Thr Asn Ser
-15 -5

Cys Pro Leu Cys Arg Tyr Glu Leu Pro Thr Asp Asp Asp Thr Tyr Glu
1 5 10 15

Glu His Arg Arg Asp Lys Ala Arg Lys Gln Gln Gln Gln His Arg Pro
20 25 30

Xaa

(2) INFORMATION FOR SEQ ID NO: 447:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Lymph ganglia
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -15..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.6

seq LILSLQVCRPATL/DQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

Met Pro Leu Ile Leu Ser Leu Gln Val Cys Arg Pro Ala Thr Leu Asp -15 -5 1

Gln Ala Thr Arg Ala Thr Thr Pro Cys Arg Leu Ser Gln Gly Cys Gln 5 10 15

Gln His Pro Thr Gln Cys Ser Thr His His Leu Thr Gln Pro Ser Pro

Trp Ala His Arg Xaa Thr Thr Arg Pro Trp Leu Glu Glu Gln Pro Arg=35 40 45

Pro Gly

121 INFORMATION FOR SEQ ID NO: 448:

- 11 SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 76 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (V1) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Surrenals
- (ix) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -73..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.6

seq LRRLLGCLTLTLS/GR

- (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 448:
- Met Leu Gly Ile Thr Ser Cys Ser Asp Gln Gln Ala Lys Glu Gly Glu
 -70 -65 -60
- Gly Leu Glu Gly Ser Ser Thr Gly Ser Ser Ser Gly Asn His Gly Gly
 -55
 -50
 -45
- Ser Gly Gly Gly Asn Gly His Lys Pro Gly Cys Glu Lys Pro Gly Asn -40 -35 -30
- Glu Ala Arg Gly Ser Gly Asn Leu Gly Phe Arg Thr Leu Arg Arg Leu -25 -15 -10
- Leu Gly Cys Leu Thr Leu Thr Leu Ser Gly Arg Ile:
 -5
- (2) INFORMATION FOR SEQ ID NO: 449:
 - (1) SEQUENCE CHARACTERISTICS:
 - A) LENGTH: 91 amino acids
 - B) TYPE: AMINO ACID
 - D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vil OBIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain

- (D) OTHER INFORMATION: score 5.6 seq ALKLASWTSMALA/AS
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

Met Ala Arg Lys Ala Leu Lys Leu Ala Ser Trp Thr Ser Met Ala Leu -15 -10 -5

Ala Ala Ser Gly Ile Tyr Phe Tyr Ser Asn Lys Tyr Leu Asp Pro Asn 1 5 10 15

Asp Phe Gly Ala Val Arg Val Gly Arg Ala Val Ala Thr Thr Ala Val 20 25 30

Ile Ser Xaa Asp Tyr Leu Thr Ser Leu Lys Ser Val Pro Tyr Gly Ser
35 40 45

Glu Glu Tyr Leu Gln Leu Arg Ser Lys Val His Leu Arg Ser Ala Arg
50 55 60

Arg Leu Cys Xaa Xaa Cys Cys Ala Asn Arg Gly 65 70

- (2) INFORMATION FOR SEO ID NO: 450:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 132 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Normal prostate
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -16..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.6

seq AALPAWLSLQSRA/RS

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:
- Met Ala Ala Ala Leu Pro Ala Trp Leu Ser Leu Gln Ser Arg Ala
 -15 -5
- Arg Ser Leu Arg Ala Phe Ser Thr Ala Val Tyr Ser Ala Thr Pro Val
- Pro Thr Pro Ser Leu Pro Glu Arg Thr Pro Gly Asn Glu Arg Pro Pro 20 25 30
- Xaa Arg Lys Ala Leu Pro Pro Arg Thr Glu Lys Met Ala Val Ass Gln 35 40 45

Asp Trp Pro Ser Val Tyr Pro Val Ala Ala Pro Xaa Lys Pro Ser Ala 50 55 60

Val Pro Leu Pro Val Arg Met Gly Tyr Pro Val Lys Lys Gly Val Pro 65 70 75 80

Met Ala Lys Glu Gly Asn Leu Glu Leu Leu Lys Ile Pro Asn Phe Leu 85 90 95

His Leu Thr Pro Val Ala Ile Lys Lys His Cys Xaa Ala Leu Lys Asp 100 105 110

Phē Cys Thr Glu 115

(2) INFORMATION FOR SEQ ID NO: 451:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 112 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (11) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Substantia nigra
- (1x) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -65..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.6 seq CMLTLXXLSFILA/GL
- (x1) SEQUENCE DESCRIPTION: SEO ID NO: 451:

Met Val Lys Ile Ala Phe Asn Thr Pro Thr Ala Val Gln Lys Glu Glu -65 -50 -55

Ala Arg Gln Asp Val Glu Ala Leu Leu Ser Arg Thr Val Arg Thr Gln -45 -40 -35

Fig. Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu Lys Glu Gly -30 -25 -20

Ala Gly Leu Ile Val Gly Gly Ala Cys Ile Tyr Lys Tyr Phe Met Pro 1 5 10

lys der Ihr Ile Tyr Arg Gly Xaa Met Cys Phe Phe Asp Ser Glu Asp

- (2) INFORMATION FOR SEQ ID NO: 452:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Thyroid
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -48..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix

602

(D) OTHER INFORMATION: score 5.6

seq LLLSFVWMPALLP/DG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

Met Ile Gly Ser Gly Leu Ala Gly Ser Gly Gly Ala Gly Gly Pro Ser
-45 -40 -35

Ser Thr Val Thr Trp Cys Ala Leu Xaa Ser Asn His Val Ala Ala Thr
-30 -25 -20

Gln Ala Ser Leu Leu Ser Phe Val Trp Met Pro Ala Leu Leu Pro
-15 -10 -5

Asp Gly Leu Pro Pro Phe Val Ala Thr Pro Met
1 5 10

- (2) INFORMATION FOR SEQ ID NO: 453:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Lung (cells)
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -18..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.6

seq LXGFLFXVIVLTS/WI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453:

Met Ser Gly Ala Gln Leu Xaa Gly Phe Leu Phe Xaa Val Ile Val Leu -15 -10 -5

Thr Ser Trp Ile Thr Ile Phe Gln Ile Tyr Arg Pro Arg Trp Gly Cys
1 5 10

Pro Trp Gly Leu Pro Leu Leu His Ile Pro Leu Gly Thr Pro Asp Asn 15 20 25 30

Phe Cys Thr Tyr

(2) INFORMATION FOR SEQ ID NO: 454:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (11) MOLECULE TYPE: PROTEIN
- (VI) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Placenta
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -29..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.6

seq VVFMTVAASGASS/FA

- (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 454:
- Met Ser Phe Phe Gln Leu Leu Met Lys Arg Lys Glu Leu Ile Pro Leu -25 -20 -15
- Val Val Phe Met Thr Val Ala Ala Ser Gly Ala Ser Ser Phe Ala Val
- Tyr Ser Leu Trp Lys Thr Asp Val Ile Leu Asp Arg Lys Lys Asn Pro
- Glu ira Trp Glu Thr Val Asp Pro Thr Val Pro Gln Lys Leu ile Thr 25 30 35
- The Ast. Glm. Glm. Trp. Lyo. Pro. He. Glu. Glu. Leu. Glm. Ast. Vol. Glm. Arg. 40. 45. 50.

Val Thr

- (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (v1) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Lung (cells)
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -15..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.5

seq LAHSLLLNEEALA/QI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455:

Met Glu Leu Ala His Ser Leu Leu Leu Asn Glu Glu Ala Leu Ala Gln
-15 -5 1

Ile Thr Glu Ala Lys Arg Pro Val Phe Ile Phe Glu Trp Leu Arg Phe 5 10 15

Leu Asp Lys Val Leu Val Ala Ala Asn Lys Thr Asp Val Lys Glu Lys 20 . 30

Gln Lys Lys Leu Val Glu Gln Leu Thr Gly Leu Ile Ser Ser Pro 35 40 45

Gly Pro Thr Gly 50

- (2) INFORMATION FOR SEQ ID NO: 456:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Prostate
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -28..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.5

seq LGYLVLSEGAVLA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456:

Met Thr Ser Ala Leu Thr Gln Gly Leu Glu Arg Ile Pro Asp Gln Leu -25 -20 -15

Gly Tyr Leu Val Leu Ser Glu Gly Ala Val Leu Ala Ser Ser Gly Asp
-10 -5 1

Leu 3lu Asn Asp Glu Gln Ala Ala Ser Ala Ile Ser Glu Leu Val Ser 5 10 15 20

Thr Ala Cys Gly Phe Arg Leu His Arg Gly Met Asn Val Pro Phe Lys 25 30 35

Arg Leu Ser Val Val Phe Gly Glu His Thr Leu Leu Val Thr Val Ser
40 45 50

Gly Gln Arg Val Phe Val Val Lys Arg Gly
55 60

(2) INFORMATION FOR SEQ ID NO: 457:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 148 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
- (1x) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -31..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.5 seq LVGVLWFVSVTTG/PW
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457:
- Met Ala Ala Trp Pro Ser Gly Pro Xaa Ala Pro Glu Ala Val Thr
 -30 -25 -20
- Ala Arg Leu Val Gly Val Leu Trp Phe Val Ser Val Thr Thr Gly Pro -15 -5 1
- Trp Gly Ala Val Ala Thr Ser Ala Gly Gly Glu Glu Ser Len Lys Cys
 5 10 15
- Giu Asp Leu Lys Val Gly Gln Tyr Ile Cys Lys Asp Pro Lys fle Asn 20 25 30
- Asp Ala Thr Gln Glu Pro Val Asn Cys Thr Asn Tyr Thr Ala His Val 35 40 45
- for the Pho Pro Ala Pro Ash Ile Thr Cys Lys Asp Xii Wir Tily Ash

Cys Arg Asn Val Asn Gly Tyr Ser Tyr Xaa Xaa Gln Xaa Xaa Val Ser 85 90 95

Phe Ser Trp Met Val Gly Ser Arg Ser Ile Leu Pro Tro Ile Pro Cys 100 105 110

Phe Gly Phe Val

- (2) INFORMATION FOR SEQ ID NO: 458:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Cancerous prostate
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -13..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.5 seq MVLLTMIARVADG/LP
 - (xi) SEQUENCE DESCRIPTION: SEO ID NO: 458:

Met Val Leu Thr Met Ile Ala Arg Val Ala Asp Gly Leu Pro Leu
-10 -5 1

Ala Ala Ser Met Gln Glu Asp Glu Gln Ser Gly Arg
5 10 15

- (2) INFORMATION FOR SEQ ID NO: 459:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 98 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Lung (cells)
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -13..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.5

seq MVLLTMIARVADG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459:

Met Val Leu Leu Thr Met Ile Ala Arg Val Ala Asp Gly Leu Pro Leu
-10 -5 1

Ala Ala Ser Met Gl
n Glu Asp Glu Gl
n Ser Gly Arg Asp Leu Gl
n Gl
n 5 $$ 10 $$ 15

Pro Thr Arg Cys Thr Leu Glu Ala Gly Ala Met Thr Phe His Tyr Ile $40 \hspace{1cm} 45 \hspace{1cm} 50$

Ile Glu Gln Gly Val Cys Tyr Leu Val Leu Cys Glu Ala Ala Phe Pro 55 60 65

Lys Lys Leu Ala Phe Ala Tyr Leu Glu Asp Leu His Ser Glu Phe Asp
70 75 80

Glu Gln 85

(2) INFORMATION FOR SEQ ID NO: 460:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 103 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (11) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Muscle
- (1x) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -69..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.4 seg MMVLSLGIXLASA/SF
- (Mi) SEQUENCE DESCRIPTION: SEQ ID NO: 460:

Met Thr Ser Gln Pro Val Pro Asn Glu Thr Ile Ile Val Leu Pro Ser
-65 -60 -55

Aun Val Ile Ash Phe Ser Gln Ala Glu Lys Pro Glu Pro Thr Ash Gln -45 -40

Xaa Leu Ala Ser Ala Ser Phe Ser Pro Asn Phe Thr Gln Val Thr Ser -5 1 5 10

Thr Leu Leu Asn Ser Ala Tyr Pro Phe Ile Gly Pro Phe Phe Phe Ile
15 20 25

Ile Ser Gly Ser Leu Ser Ile 30

(2) INFORMATION FOR SEQ ID NO: 461:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 135 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Placenta
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -25..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.3

seq AVTSLLSPTPATA/LA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461:

Met Ala Ser Val Val Leu Ala Leu Arg Thr Arg Thr Ala Val Thr Ser -25 -15 -10

Leu Leu Ser Pro Thr Pro Ala Thr Ala Leu Ala Val Arg Tyr Ala Ser
-5 1 5

Lys Lys Ser Gly Gly Ser Ser Lys Asn Leu Gly Gly Lys Ser Ser Gly
10 15 20

Arg Arg Gln Gly Ile Lys Lys Met Glu Gly His Tyr Val His Ala Gly 25 30 35

Asn Ile Ile Ala Thr Gln Arg His Phe Arg Trp His Pro Gly Ala His 40 45 50 55

Val Gly Val Gly Lys Xaa Lys Cys Leu Tyr Ala Leu Glu Glu Gly Ile 60 65 70

Val Arg Tyr Thr Lys Glu Val Tyr Val Pro His Pro Arg Asn Thr Glu
75 80 85

Ala Val Xaa Leu Ile Thr Arg Leu Kaa Lys Gly Ala Val Leu Tyr Lys 90 95 100

Thr Phe Val Thr Trp Phe Leu 105 110

(2) INFORMATION FOR SEQ ID NO: 462:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 135 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MCLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Substantia nigra
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -25..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (C:) OTHER INFORMATION: score 5.3

seq AVTSLLSPTPATA/LA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 462:

Met Ala Ser Val Val Leu Ala Leu Arg Thr Arg Thr Ala Val Thr Ser -25 -20 -15 -10

Leu Leu Ser Pro Thr Pro Ala Thr Ala Leu Ala Val Arg Tyr Ala Ser
-5 1 5

Lys Lys Ser Gly Gly Ser Ser Lys Asn Leu Gly Gly Lys Ser Ser Gly
10 15 20

Arg Arg Gln Gly Ile Lys Lys Met Glu Gly His Tyr Val His Ala Gly
25 30 35

Ash Ile Ile Ala Thr Gln Arg His Phe Arg Trp His Pro Gly Ala His 40 50 55

Val Gly Val Gly Lys Asn Lys Cys Leu Tyr Ala Leu Glu Glu Gly Ile 60 65 70

Mad Arg Tyr Thr Lys Glu Val Tyr Val Pro His Pro Arg Asn Thr Glu
75 80 85

Al: Val App Leu Ile Thr Arg Leu Pro Lys Gly Ala Val Lau Tyr Lys 95 100

Thr Phe Val His Val Val Pro 105 110

". IMPORMATION FOR SEQ ID NO: 463:

- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
- (ix) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -57..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.3

seq AIALATVLFLIGA/FL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463:

Met Met Pro Ser Arg Thr Asn Leu Ala Thr Gly Ile Pro Ser Ser Lys
-55 -50 -45

Val Lys Tyr Ser Arg Leu Ser Ser Thr Asp Asp Gly Tyr Ile Asp Leu
-40 -35

Gln Phe Lys Lys Thr Pro Pro Lys Ile Pro Tyr Lys Ala Ile Ala Leu
-25 -15 -10

Ala Thr Val Leu Phe Leu Ile Gly Ala Phe Leu Ile Ile Gly Ser
-5 1 5

Leu Leu Ser Gly Tyr Ile Ser Lys Gly Gly Ala Asp Arg Ala Val 10 15 20

Pro Val Leu Ile Ile Gly Ile Leu Val Phe Leu Pro Gly Phe Tyr His 25 30 35

- (2) INFORMATION FOR SEO ID NO: 464:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Testis
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -15..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.6 seq LILSLQVCRPATL/DQ
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:

-15

-10

- 5

1

Gln Ala Thr Arg Ala Thr Thr Pro Cys Arg Leu Ser Gln Gly Cys Gln
5 10 15

Gln His Pro Thr Xaa Gln 20

- (2) INFORMATION FOR SEQ ID NO: 465:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (11) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Testis
 - (ix) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -15..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.6

seq LILSLQVCRPATL/DQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465:

Met Pro Leu Ile Leu Ser Leu Gln Val Cys Arg Pro Ala Thr Leu Asp -15 -5 1

Gln Ala Thr Arg Ala Thr Thr Pro Cys Arg Leu Ser Gln Gly Cys Gln
5 10 15

White is a walter of the control of

Gin His Pro Thr Gln Cys Ser Thr His Leu Gly 20 25

- (2) INFORMATION FOR SEQ ID NO: 466:
 - (1) SEQUENCE CHARACTERISTICS:
 - (A. LENGTH: 81 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (11) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain

- (D) OTHER INFORMATION: score 5.2 seq GVLLLLSSIHFQC/RR
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466:

Met Ala Ser Ser Val Gly Asn Val Ala Asp Ser Thr Glu Pro Thr Lys -65 -60 -55

Arg Met Leu Ser Phe Gln Gly Leu Ala Glu Leu Ala His Arg Glu Tyr -50 -45 -40

Gln Ala Gly Asp Phe Glu Ala Ala Glu Arg His Cys Met Gln Leu Trp
-35 -30 -25

Arg Gln Glu Pro Asp Asn Thr Gly Val Leu Leu Leu Leu Ser Ser Ile
-20 -15 -10 -5

His Phe Gln Cys Arg Arg Leu Asp Arg Ser Ala His Phe Ser Thr Leu $1 \hspace{1cm} 5 \hspace{1cm} 10$

Ala

- (2) INFORMATION FOR SEQ ID NO: 467:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 110 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -94..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5 seq VILQLQFLFDVLQ/KT
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467:

Met Phe Gly Ser Ala Pro Gln Arg Pro Val Ala Met Thr Thr Ala Gln
-90 -85 -80

Arg Asp Ser Leu Leu Trp Lys Leu Ala Gly Leu Leu Arg Glu Xaa Gly
-75 -70 -65

Asp Val Val Leu Ser Gly Cys Ser Thr Leu Ser Leu Leu Thr Pro Thr
-60 -55 -50

Leu Gln Gln Leu Asn His Val Phe Glu Leu His Leu Gly Pro Trp Gly -45 -40 -35

Pro Gly Gln Thr Gly Phe Val Ala Leu Pro Ser His Pro Ala Asp Ser

-30

-25

-20

-15

Pro Val Ile Leu Gln Leu Gln Phe Leu Phe Asp Val Leu Gln Lys Thr
-10 -5 1

Leu Ser Leu Lys Leu Val His Val Ala Gly Pro Gly Pro Thr 5 10 15

(2) INFORMATION FOR SEQ ID NO: 468:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -86..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5 seq LILVGTSKHVAFG/KI
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468:

Met Ser Phe Ile Phe Glu Trp Ile Tyr Asn Gly Phe Ser Ser Val Leu -85 -80 -75

Gln Phe Leu Gly Leu Tyr Lys Lys Ser Gly Lys Leu Val Phe Leu Gly
-70 -65 -60 -55

Leu Asp Asn Ala Gly Lys Thr Thr Leu Leu His Met Leu Lys Asp Asp -50 -45 -40

Arg Leu Gly Gln His Val Pro Thr Leu His Pro Thr Ser Glu Glu Leu
-35 -30 -25

Thr Ile Ala Gly Met Thr Leu Gln Leu Leu Ile Leu Val Gly Thr Ser -20 -15 -10

Lys His Val Ala Pho Gly Lys Ile Ile -i 1

-0" INFORMATION FOR SEQ ID NO: 469:

: SEQUENCE CHARACTERISTICS:

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Cancerous prostate
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -35..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5

seq WYSTVGLLPPVRA/MS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469:

Met Asp Lys Pro Cys Gly Cys Pro Pro Gly Val Cys Asp His Gly Thr -35 -25 -20

Gly Asp Arg Arg Asp Pro Trp Tyr Ser Thr Val Gly Leu Leu Pro Pro
-15 -10 -5

Val Arg Ala Met Ser Gln Arg Asn Leu Asn
1 5

- (2) INFORMATION FOR SEO ID NO: 470:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 134 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Testis
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -36..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5

seq ARALAALVPGVTQ/VD

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:
- Met Ala Ala Leu Lys Cys Leu Leu Thr Leu Gly Arg Trp Cys Pro
 -35 -30 -25
- Gly Leu Gly Val Ala Pro Gln Ala Arg Ala Leu Ala Ala Leu Val Pro
 -20 -15 -10 -5
- Gly Val Thr Gln Val Asp Asn Lys Ser Gly Phe Leu Gln Lys Arg Pro 1 5 10
- His Arg Gln His Pro Gly Ile Leu Lys Leu Pro His Val Arg Leu Pro
 15 20 25

Gln Ala Leu Ala Asn Gly Ala Gln Leu Leu Leu Leu Gly Ser Ala Gly 30 35 40

Pro Thr Met Glu Asn Gln Val Gln Thr Leu Thr Ser Tyr Leu Trp Ser 45 50 55 60

Arg His Leu Pro Val Glu Pro Xaa Glu Leu Gln Arg Arg Ala Xaa His 65 70 75

Led Glu Lys Lys Phe Leu Glu Asn Pro Asp Leu Ser Gln Thr Glu Glu 80 85 90

Lys Leu Arg Gly Ala Gly 95

(2) INFORMATION FOR SEQ ID NO: 471:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 117 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (11) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Normal prostate
- (1x) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -102..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.9

seq TVMSALSVAPSKA/RE

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471:
- Met Val Ala Arg Val Trp Ser Leu Met Arg Phe Leu Ile Lys Gly Ser
 -100 -95 -90
- Val Ala Gly Gly Ala Val Tyr Leu Val Tyr Asp Gln Glu Leu Leu Gly -85 -80 -75
- Erg Ser Asp Lys Ser Gln Ala Ala Leu Gln Lys Ala Gly Glu Val Val -65 -60 -55
- er. Fro Ala Met Xaa Gln Phe Ser Gln Tyr Val Cys Gln Gln Thr Gly
 -50 -45 -40
- Leu Gln Ile Pro Gln Leu Pro Ala Pro Pro Lys Ile Tyr Phe Pro Ile
 -35 -30 -25
- and And Ser Orp Xaa Ala Gly Ile Met Thr Val Met Ser Ala Leu Ser

Val Lys Ala Leu Gly 15

- (2) INFORMATION FOR SEQ ID NO: 472:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -16..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.9

seq ELQNLXSLQGSQA/CS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472:

Cys Ser Ser Ser Lys Gln Arg Phe 1 5

- (2) INFORMATION FOR SEQ ID NO: 473:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -24..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.9

seq FFFSIQPFLPCSS/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473:

Met Leu Tyr Met Ser Leu Lys Tyr Ile Arg Ala Phe Phe Phe Ser Ile

-10

-15

-20

Oln Pro Phe Leu Pro Cys Ser Ser Arg Pro Leu Lys Ser Pro Ser Pro

Val Ala His Pro Thr Asn Ile Ser Val Ser Glu Asn Ala Gln Arg Cys
10 20

Leu Xaa Thr Ser Pro Trp 28 30

(2) INFORMATION FOR SEQ ID NO: 474:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Cancerous prostate
- (1x) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -79..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.9

seq WVIVLTSWITIFQ/IY

- (X1) SEQUENCE DESCRIPTION: SEQ ID NO: 474:
- Met Asn Leu Glu Arg Val Ser Asn Glu Glu Lys Leu Asn Leu Cys Arg
 -75 -70 -65
- Lys Tyr Tyr Leu Gly Gly Phe Ala Phe Leu Pro Phe Leu Trp Leu Val -60 -55 -50
- Asn Ile Phe Trp Phe Phe Arg Glu Ala Phe Leu Val Pro Ala Tyr Thr -45 -40 -35
- Gl. Gln Ser Gln Ile Lys Gly Tyr Val Trp Arg Ser Ala Val Gly Phe -30 -20
- Led and Trp Val Ile Wal Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile -1. +5 1
- Tyr Arg Pro Arg Trp Gly Ala Leu Gly Asp Xaa Leu Ser Phe Thr Ile
 5 10 15
- It led Gly Thr Pro Asp Ash Phe Cys Par Tyr

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -70..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.9

seq LVFVLLFIFVKRQ/IM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475:

Met Ala Gly Glu Leu Gln Gly Thr Gln Ala Pro Ser Leu Arg Gly Xaa -70 -65 -60 -55

- Gly Leu Thr Ser Gln Asp Ser Gly Val Asn Pro Asn Asn Ser Xaa Arg
 -50 -45 -40
- Gly Arg Glu Ala Met Ala Ser Gly Ser Asn Trp Leu Ser Gly Val Asn
 -35
 -30
 -25
- Val Val Leu Val Met Ala Tyr Gly Ser Leu Val Phe Val Leu Leu Phe
 -20 -15 -10
- Ile Phe Val Lys Arg Gln Ile Met Arg Phe Ala Met Lys Ser Arg Arg
 -5 1 5 10
- Gly Pro His Val Pro Val Gly Xaa Gln Cys Pro Gln Xaa Cys Tyr Asn 15 20 25

Tyr Leu Tyr

- (2) INFORMATION FOR SEQ ID NO: 476:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Normal prostate
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -56..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.9

seq FACVPGASPTTLA/FP

(X1) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

Met Thr Gly Phe Leu Leu Pro Pro Ala Ser Arg Gly Thr Arg Arg Ser
-55 -50 -45

Cys Ser Arg Ser Arg Lys Arg Gln Thr Arg Arg Arg Arg Asn Pro Ser -45 -35 -30 -25

Ser Phe Val Ala Ser Cys Pro Thr Leu Leu Pro Phe Ala Cys Val Pro
-20 -15 -10

3iy Ala Ser Pro Thr Thr Leu Ala Phe Pro Pro Val Val Leu Thr Gly
-5
5

Pro Ser Thr Asp Gly Ile Pro Phe Ala Leu Ser Leu Gln Arg Val Pro 10 15 20

Pne Val 25

(2) INFORMATION FOR SEQ ID NO: 477:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 76 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -26..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.9 seq VLCTNQVLITARA/VP
- %x1) SEQUENCE DESCRIPTION: SEQ ID NO: 477:
- Inc Ash Gln Val Leu Ile Thr Ala Arg Ala Val Pro Thr Lys Lys Ala
- on Ma. And Cos Mal Xaa Lys And Dep Trp Ile Pro Lys Thr Thr Ser

Phe Thr Phe Cys Leu Glu Phe Ser Arg His Arg Cys
40 45 50

- (2) INFORMATION FOR SEQ ID NO: 478:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Hypertrophic prostate
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -17..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.8

seq LXXVVAFVAPGES/QQ

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478:
- Met Val Arg Arg Leu Xaa Xaa Val Val Ala Phe Val Ala Pro Gly Glu
 -15 -10 -5
- Ser Gln Gln Glu Glu Pro Pro Thr Asp Asn Gln Asp Ile Glu Pro Gly
 1 5 10 15
- Gln Glu Arg Glu Gly Thr Pro Pro Ile Glu Glu Arg Lys Val Glu Gly
 20 25 30
- Asp Cys Gln Glu Met Asp Leu Glu Lys Thr Arg Ser Glu Arg Gly Asp 35 40 45
- Gly Ser Asp Val Lys Glu Lys Thr Pro Pro Asn Xaa Lys His Ala Lys 50 55 60
- Thr Lys Glu Ala Gly Asp Gly Pro Leu 65 70
- (2) INFORMATION FOR SEQ ID NO: 479:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 149 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Lung (cells)

- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -37..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.8

seq PIVRLLSCPGTVA/KD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479:

Met Ala Val Pro Gly Val Gly Leu Leu Thr Arg Leu Asn Leu Cys Ala
-35 -30 -25

Arg Arg Arg Thr Arg Val Gln Arg Pro Ile Val Arg Leu Leu Ser Cys
-20 -15 -10

Pro Gly Thr Val Ala Lys Asp Leu Arg Arg Asp Glu Gln Pro Ser Gly -5 1 5 10

Ser Val Glu Thr Gly Phe Glu Asp Lys Ile Pro Lys Arg Arg Phe Ser 15 20 25

Glu Met Gln Asn Glu Arg Arg Glu Gln Ala Gln Arg Thr Val Leu Ile 30 35 40

His Cys Pro Glu Lys Ile Ser Glu Asn Lys Phe Xaa Lys Tyr Leu Ser 45 50 55

Gln Phe Gly Pro Ile Asn Asn His Phe Phe Tyr Glu Ser Phe Gly Leu 60 70 75

Tyr Ala Val Val Glu Phe Cys Gln Lys Glu Ser Ile Gly Ser Leu Gln 80 85 90

Ash Gly Thr His Thr Pro Ser Thr Ala Met Glu Thr Ala Ile Pro Phe 95 100 105

Arg Ser Arg Ser Ser 110

- (2) INFORMATION FOR SEQ ID NO: 480:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 103 amino acids
 - (B) TYPE: AMINO ACID
 - (1), TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Lymph ganglia
 - :x: FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480:

Met Met Ala Ala Val Pro Pro Gly Leu Glu Pro Trp Asn Arg Val Arg
-60 -55 -50 -45

Ile Pro Lys Ala Gly Asn Arg Ser Ala Val Thr Val Gln Asn Pro Gly
-40 -35 -30

Ala Ala Leu Asp Leu Cys Ile Ala Ala Val Ile Lys Glu Cys His Leu
-25 -20 -15

Val Ile Leu Ser Leu Lys Ser Gln Thr Leu Asp Ala Glu Thr Asp Val $-10 \\ \hspace{1.5cm} -5 \\ \hspace{1.5cm} 1$

Leu Cys Ala Val Leu Tyr Ser Asn His Asn Arg Met Gly Arg His Lys 5 10 15 20

Pro His Leu Ala Leu Lys Gln Val Glu Gln Cys Leu Lys Arg Leu Xaa 25 30 35

Asn Met Asn Leu Glu Gly Gly 40

(2) INFORMATION FOR SEQ ID NO: 481:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -33..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.8 seq SLVHLLCQNQVLG/NP
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481:

Met Ala Ser Leu Asp Arg Val Lys Val Leu Val Leu Gly Asp Ser Gly -30 -25 -20

Val Gly Lys Ser Ser Leu Val His Leu Cys Gln Asn Gln Val Leu
-15 -10 -5

Gly Asn Pro Ser Trp Thr Val Gly Cys Ser Val Asp Val Arg Val His 1 5 10

Asp Tyr Lys Glu Gly Thr Pro Glu Glu Lys Thr Tyr Tyr Ile Glu Leu 20 25 30

Trp Asp Val Gly Gly Ser Val Gly Ser Ala Ser Ser Val Lys Ser Thr 35 40° 45

Arg Ala Val Phe Tyr Asn Ser Val Asn Gly Ile Ile Xaa Val His Asp
50 55 60

Led Thr Maa Gly Lys Ser Ser Gln Maa Leu Arg Arg Trp Ser Leu Glu 65 70 75

Ala Lea Asn Arg Asp Leu Val Pro Thr Gly Val Leu Val 80 90

(2) INFORMATION FOR SEQ ID NO: 482:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (11) MGLECULE TYPE: PROTEIN
- (vi) OFIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -31..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.8 seq WAFSCGTWLPSRA/EW
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482:
- Mot Val Phe Pro Ala Lys Arg Phe Cys Leu Val Pro Ser Met Glu Gly -30 -25 -20
- Val Arg Trp Ala Phe Ser Cys Gly Thr Trp Leu Pro Ser Arg Ala Glu
 -15 -5 1
- Trp Leu Leu haa Val Arg Ser Ile Gln Pro Glu Glu Lys Glu Arg Ile
 5 10 15
- Hij Jun Phe Val Phe Ala Arg Hop Ala Lys Ala Ala Met Ala Gly Arg 25 30

Led Met Ile Arg Lys Led Val Ala Glu Ash Arg

LARGRIATION FOR SEQ IC : 1 483.

- (ii) MOLECULE TYPE: PROTEIN
- (vi) OFIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Surrenals
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -26..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.7

seq LIMQLGSVLLTRC/PF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483:

Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln Leu Ile Met

Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly Cys Phe
-10 -5 1 5

Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg Lys Pro 10 15 20

Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala Ala Val Leu 25 30 35

Cys Ala Arg 40

- (2) INFORMATION FOR SEQ ID NO: 484:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 amino acids
 - (B) TYPE: AMING ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -31..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.7

seq LAVDSWWLDPGHA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484:

Met Leu Ser Lys Gly Leu Lys Arg Lys Arg Glu Glu Glu Glu Glu Lys -30 -25

Glu Pro Leu Ala Val Asp Ser Trp Trp Leu Asp Pro Gly His Ala Ala

-5

1

Val Ala Gin Ala Pro Pro Ala Val Ala Ser Ser Ser Leu Phe Asp Leu
5 10 15

Ser Val Leu Lys Leu His His Ser Arg Gly 20 25

- (2) INFORMATION FOR SEQ ID NO: 485:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
 - (ix) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -16..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.7 seq SLAAALTLHGHWG/LG
 - (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 485:

Met Asp Tyr Ser Leu Ala Ala Leu Thr Leu His Gly His Trp Gly
-15 -5

Leu Gly Gln Val Val Thr Asp Tyr Val His Gly Asp Ala Leu Gln Lys
1 5 10 15

Ala

- (2) INFORMATION FOR SEQ ID NO: 486:
 - (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 84 amino acids
 - 131 TYPE: AMINO ACID
 - ID, TOPOLOGY: LINEAR
 - ily MCLECULE TYPE: PROTEIN
 - .vi/ OFIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal

- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7

seq LSLXASYIFGISG/FE

(X1) SEQUENCE DESCRIPTION: SEQ ID NO: 486:

Met Ser Tyr Ile Thr Ser Gln Glu Met Lys Cys Ile Leu His Trp Phe
-70 -65 -60

Ala Asn Trp Ser Gly Pro Gln Arg Glu Arg Phe Leu Glu Asp Leu Val
-55 -45

Ala Lys Ala Val Pro Glu Lys Leu Gln Pro Xaa Leu Asp Ser Leu Glu -40 -35 -30 -30

Gln Leu Ser Val Ser Gly Ala Asp Asp His Leu Leu Ser Leu Xaa Ala -20 -15 -10

Ser Tyr Ile Phe Gly Ile Ser Gly Phe Glu Ala Gly Ala Glu Gln Glu -5 1 5

Arg Asn Glu Phe Val Arg Gln Ser

- (2) INFORMATION FOR SEQ ID NO: 487:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
 - (ix) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -76..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.7

seq LIVYLWVVSFIAS/SS

- (Mi) SEQUENCE DESCRIPTION: SEQ ID NO: 487:
- Met Pro Leu Leu Cys Gln Ile Glu Met Glu Tyr Leu Leu Lys Trp
 -75 -70 -65
- Gln Met Thr Met Leu Gln Ser Met Leu Cys Asp Leu Val Ser Tyr Pro
 -60 -55 -50 -50 -45
- Leu Leu Pro Leu Gln Gln Thr Lys Glu Ala Asn Leu Asp Phe Pro Lys
 -40 -35 -30
- Ile Lys Val Ser Ser Val Thr Ile Thr Pro Thr Arg Trp Phe Xaa Leu -25 -20 -15

Ile Val Tyr Leu Trp Val Val Ser Phe Ile Ala Ser Ser Ser -10 -5 1

(2' INFORMATION FOR SEQ ID NO: 488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (v1) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Surrenals
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -22..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.7

seq SVMGVCLLIPGLA/TA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488:

Met Trp Phe Glu Ile Leu Pro Gly Leu Ser Val Met Gly Val Cys Leu
-20 -15 -10

Len Ile Pro Gly Leu Ala Thr Ala Tyr Ile His Xaa Phe Thr Asn Arg
-5 1 5 10

Gly Lys Glu Lys Arg Val Ala His Phe Gly Tyr His Trp Ser Leu Met
15 20 25

Thu Arg Asp Arg Arg Ile Ser Gly Val Asp Arg Tyr Tyr Val Ser Lys 30 35 40

Ul : / Gly 45

DESENATION FOR SEQ ID NO: 489:

UEQUENCE CHARACTERISTICS:

[A] LENGTH: 50 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

.. MOLECULE TYPE: PROTEIN

H. MIGINAL SOURCE:

- (B) LOCATION: -46..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6 seq LLVSLVLRXPAKS/TR
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489:

Met Glu Phe Lys Leu Glu Ala His Arg Ile Val Ser Ile Ser Leu Gly -45 -40 -35

Lys Ile Tyr Asn Ser Arg Val Gln Arg Gly Gly Ile Lys Leu His Lys
-30 -25 -20 -15

Asn Leu Leu Val Ser Leu Val Leu Arg Xaa Pro Ala Lys Ser Thr Arg
-10 -5 1

Ala Gly

- (2) INFORMATION FOR SEQ ID NO: 490:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 109 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (i1) MOLECULE TYPE: PROTEIN
 - (V1) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
 - (i::) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -97..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.6

seg IASGLGLXLDCWT/SS

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490:
- Met Ala Val Leu Ser Lys Glu Tyr Gly Phe Val Leu Leu Thr Gly Ala
 -95 -90 -85
- Aid Ser Phe Ile Met Val Ala His Leu Ala Ile Asn Val Ser Lys Ala
 -80 -75 -70
- Ary Lys Lys Tyr Lys Val Glu Tyr Pro Ile Met Tyr Ser Thr Asp Pro -65 -60 -55 -50
- Glu Asn Gly His Ile Phe Asn Cys Ile Gln Arg Ala His Gln Asn Thr
 -45 -40 -35
- Lota Glu Mal Tyr Pro Xaa Phe Leu Phe Phe Leu Ala Val Gly Gly Val -30 -25 -20
- Ov. Als Pro Arg Ile Ala Ser Gly Leu Gly Leu Xaa Leu Asp Cys Trp -15 -10 -5

The Ser Ser Leu Cys Leu Trp Leu Leu His Gly Pro Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 491:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -42..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.6

seq RIPSLPGSPVCWA/WP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

Met Asp Gly His Trp Ser Ala Ala Phe Ser Ala Leu Thr Val Thr Ala -40 -35 -30

Net Ser Ser Trp Ala Arg Arg Ser Ser Ser Ser Arg Arg Ile Pro
-25 -20 -15

Ser Leu Pro Gly Ser Pro Val Cys Trp Ala Trp Pro Trp

IMFORMATION FOR SEQ ID NO: 492:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- 11 MOLECULE TYPE: PROTEIN
- vis URIGINAL SOURCE:
 - (A) OFGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Liver
- IM FEATURE:
 - (A) NAME/KEY: sig peptide

g garan Tagaran dan dan Tabub dan Kebagai

B) LOCATION. -16..-1

Met Ala Gln Arg Leu Leu Leu Arg Arġ Phe Leu Ala Ser Val Ile Ser -15 -5

Arg Lys Pro Ser Gln Gly Gln Trp Pro Pro Leu Thr Ser Arg Ala Leu 1 5 10 15

Gln Thr Pro Gln Cys Ser Pro Gly Gly Leu Thr Val Thr Pro Asn Pro 20 25 30

Ala Arg Thr 35

- (2) INFORMATION FOR SEQ ID NO: 493:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Lymph ganglia
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -25..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.5 seq FLLLLEVSHLLLI/IN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493:

Met Ala Ser Leu Lys Pro Ala Phe Val Asn Tyr Phe Phe Leu Leu Leu -25 -10 -10

Leu Glu Val Ser His Leu Leu Leu Ile Ile Asn Ala Glu Gly
-5 1 5

- (2) INFORMATION FOR SEQ ID NO: 494:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 amino acids
 - (3) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Substantia nigra
 - (1x) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -77..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5

seq LFWVIVLTSWITI/FQ

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 494:

Mat Asn Leu Glu Arg Val Ser Asn Glu Glu Lys Leu Asn Leu Cys Arg -75 -70 -65

Lys Tyr Tyr Lau Gly Gly Phe Ala Phe Leu Pro Phe Leu Trp Leu Val -60 -55 -50

Asn Ile Phe Trp Phe Phe Arg Glu Ala Phe Leu Val Pro Ala Tyr Thr
-45 -35 -30

Glu Gln Ser Gln Ile Lys Gly Tyr Val Trp Arg Ser Ala Val Gly Phe
-25 -20 -15

Lou Phe Trp Val Ile Val Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile -10 -5 1

(2) INFORMATION FOR SEQ ID NO: 495:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (v1) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Lung (cells)
- (ix) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -21..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.4

seg AVASSFFCASLFS/AV

(xill SEQUENCE DESCRIPTION: SEQ ID NO: 495:

11 1 Als Cln Lep Gly Als Val Val Ala Val Ala Ser Ser Phe Phe Cys -20 -15 -10

Als Ser Leu Phe Ser Ala Val His Lys Ile Glu Glu Gly His Ile Gly

1 5 10

🐃 ... The Tyr Arg Gly Gly Val

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -25..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.4

seq LVFMVPLVGLIHL/GW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496:

Met Ser Leu Arg Asn Leu Trp Arg Asp Tyr Lys Val Leu Val Phe Met
-25 -10 -10

Val Pro Leu Val Gly Leu Ile His Leu Gly Trp Tyr Arg Ile Lys Ser -5 1 5

Ser Pro Val Phe Gln Ile Pro Lys Asn Asp Asp Ile Pro Glu Gln Asp 10 15 20

Ser Leu Gly Leu Ser Asn Leu Gln Lys Ser Gln Ile Gln Gly Ile Leu 25 30 35

- (2) INFORMATION FOR SEQ ID NO: 497:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Spleen
 - (ix) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -23..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.4

seq VFCLLISIPTPSA/HL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497:

Net Gly Trp Asp Gly Cys Lys Cys Leu Gly Val Phe Cys Leu Leu Ile

-20 -15 -10

Ser Ile Pro Thr Pro Ser Ala His Leu -5

13: INFORMATION FOR SEQ ID NO: 498:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 149 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (11) MOLECULE TYPE: PROTEIN
- (V1) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -118..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.4 seq ILAHRLGLIPIHA/DP
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498:
- Met Ala Ala Ser Gln Ala Val Glu Glu Met Arg Thr Ala Trp Phe Trp
 -115 -110 -105
- Gly Ser Leu Gly Phe Ala Met Ser Ile Leu Leu Thr Phe Pro Val Thr -100 -95 -90
- Ile Pro Val Met Met Met Pro Gly Thr Arg Xaa Gly Phe Glu Xaa Arg
 -85 -80 -75
- Maa Phe Arg Val Asp Val Val His Met Asp Glu Asn Ser Leu Glu Phe -70 -65 -60 -55
- Asp Met Val Gly Ile Asp Ala Ala Ile Ala Asn Ala Phe Arg Arg Ile
 -50 -45 -40
- In: Lou Ala Glu Val Pro Thr Met Ala Val Glu Lys Val Leu Val Tyr +35 -30 -25
- Ash Ash Thr Ger Ile Val Gln Asp Glu Ile Leu Ala His Arg Leu Gly -20 -15 -10
- Leu Ile Pro Ile His Ala Asp Pro Arg Leu Phe Glu Tyr Arg Asm Glm -5 10
- 1. Arm 312 310 Gly Thr Glu 110 Asp Thr Leu Gln Phe Arg Leu Gln

- (2) INFORMATION FOR SEQ ID NO: 499:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 124 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Muscle
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -77..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.4

seq FEARIALLPLLQA/ET

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499:
- Met Ala Ala Ser Lys Val Lys Gln Asp Met Pro Pro Pro Gly Gly Tyr
 -75
 -70
 -65
- Gly Pro Ile Asp Tyr Lys Arg Asn Leu Pro Arg Arg Gly Leu Ser Gly -60 -55 -50
- Tyr Ser Met Leu Ala Ile Gly Ile Gly Thr Leu Ile Tyr Gly His Trp
 -45 -30 -35
- Ser Ile Met Lys Trp Asn Arg Glu Arg Arg Arg Leu Gln Ile Glu Asp
 -25 -20 -15
- Phe Glu Ala Arg Ile Ala Leu Leu Pro Leu Leu Gln Ala Glu Thr Asp
 -10 -5 1
- Arg Xaa Thr Leu Gln Met Leu Arg Glu Asn Leu Glu Glu Glu Ala Ile 5 10 15
- Ile Met Xaa Asp Val Xaa Asp Trp Xaa Val Gly Xaa Xaa Xaa Val Pro 20 25 30 35
- His Asn Pro Leu Gly Ala Pro Leu Asp Arg Gly Ala
 40
 45
- (2) INFORMATION FOR SEQ ID NO: 500:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -42..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.4

seq VLFFTGWWIIIDA/AV

(M1) SEQUENCE DESCRIPTION: SEQ ID NO: 500:

Met Ser Gly Phe Leu Glu Gly Leu Arg Cys Ser Glu Cys Ile Asp Trp
-40 -35 -30

Gly Glu Lys Arg Asn Thr Ile Ala Ser Ile Ala Ala Gly Val Leu Phe
-25
-20
-15

Phe Thr Glv Trp Trp Ile Ile Ile Asp Ala Ala Val Ile Tyr Pro Thr -10 -5 1 5

Arg

- (2) INFORMATION FOR SEQ ID NO: 501:
 - (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (v1) OFIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
 - (1x) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -44..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.4 seq LVFLTFLSIPSFV/GL
 - (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 501:
- Not Mat THE SEE Glu Pro Gly Ile Tyr Thr Trp Pro Glu Lys Thr Arg
 -40 -35 -30
- Tie He Cys Ser Ala Cys Ser Ser Val Pro Leu Pro Trp Thr Val Leu
 -25 -20 -15
- in the in: The Phe Leu Ser Ile Pro Ser Phe Val Gly Leu Ard Ash

- (2) INFORMATION FOR SEQ ID NO: 502:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 140 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Substantia nigra
 - (ix) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -14..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.4

seq FLTALLWRGRIPG/RQ

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:
- Met Phe Leu Thr Ala Leu Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln
 -10 -5 1
- Trp Ile Gly Lys His Arg Arg Pro Arg Phe Val Ser Leu Arg Ala Lys
 5 10 15
- Gln Asn Met Ile Arg Arg Leu Glu Ile Glu Ala Glu Asn His Tyr Trp 20 25 30
- Leu Ser Met Pro Tyr Met Thr Arg Glu Gln Glu Arg Gly His Ala Xaa 35 40 45 50
- Leu Arg Arg Arg Glu Ala Phe Glu Ala Ile Lys Ala Ala Ala Thr Ser
 55 60 65
- Lys Phe Pro Pro His Arg Phe Ile Ala Asp Gln Leu Asp His Leu Xaa 70 75 80
- Xaa His Gln Glu Met Val Leu Ile Leu Ser Arg His Pro Trp Ile Leu 85 90 95
- Trp Ile Thr Glu Leu Thr Ile Phe Thr Trp Ser Gly Leu Lys Asn Cys 100 105 110
- Ser Leu Cys Glu Asn Glu Leu Trp Thr Ser Leu Tyr 115 120 125
- (2) INFORMATION FOR SEQ ID NO: 503:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR

- (11) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens(D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -90..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.3

seq TCLTACWTALCCC/CL

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 503:

Met Asn Gln Glu Asn Pro Pro Pro Tyr Pro Gly Pro Gly Pro Thr Ala -90 -85 -80 -75

Pro Tyr Pro Pro Tyr Pro Pro Gln Pro Met Gly Pro Gly Xaa Met Gly
-70 -65 -60

Gly fro Tyr Pro Pro Pro Gln Gly Tyr Pro Tyr Gln Gly Tyr Pro Gln
-55 -50 -45

Tyr Gly Trp Gln Gly Gly Pro Gln Glu Pro Pro Lys Thr Thr Val Tyr
-40 -35 -30

Val Val Glu Asp Gln Arg Arg Asp Glu Leu Gly Pro Ser Thr Cys Leu
-25 -20 -15

Thr Ala Cys Trp Thr Ala Leu Cys Cys Cys Leu Trp -10 -5 1

- (2) INFORMATION FOR SEQ ID NO: 504:
 - (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 119 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MCLECULE TYPE: PROTEIN
 - [V1] ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - #U) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
 - 'lky FEATURE:
 - (A) NAME/KEY: sig_peptide
 - 'B) LOCATION: -54..-1
 - 1 IDENTIFICATION METHOD: Von Heijne matrix
 - 10: CTHER INFORMATION: score 4.3

Met Ala Ser Leu Glu Val Ser Arg Ser Pro Arg Arg Ser Arg Glu -50 -45 -40

Leu Glu Val Arg Ser Pro Arg Gln Asn Lys His Ser Val Leu Leu Pro
-35 -30 -25

Thr Tyr Asn Glu Arg Glu Glu Leu Pro Leu Ile Val Trp Leu Leu Val -20 -15 -10

Lys Ser Phe Ser Glu Ser Gly Ile Asn Tyr Glu Ile Ile Ile Ile Asp -5 10

Asp Gly Ser Pro Asp Gly Thr Arg Asp Val Ala Glu Gln Leu Glu Lys
15 20 25

Ile Tyr Gly Ser Asp Arg Ile Leu Leu Arg Pro Arg Glu Lys Lys Leu 30 35 40

Gly Leu Gly Thr Ala Tyr Ile His Gly Met Xaa Thr Cys His Arg Xaa 45 50 55

Leu His His Tyr Tyr Gly Cys
60 65

(2) INFORMATION FOR SEQ ID NO: 505:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Hypertrophic prostate
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -14..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.2 seq CPTCLCAPSXXWG/EP
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505:

Met Cys Pro Thr Cys Leu Cys Ala Pro Ser Xaa Xaa Trp Gly Glu Pro
-10 -5 1

Val Gly Ser Pro Gly Leu Ser Ser Pro Val Leu Ser Pro Ser Lys Lys
5 10 15

Ala Arg Ser 20

(2) INFORMATION FOR SEQ ID NO: 506:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MCLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -19..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.2 seq AVAASAASQAEG/KK
- (X1) SEQUENCE DESCRIPTION: SEQ ID NO: 506:
- Met Ala Ala Ala Thr Gly Ala Val Ala Ala Ser Ala Ala Ser Gly Gln
 -15 -10 -5
- Ala Glu Gly Lys Lys Ile Thr Asp Leu Arg Val Ile Asp Leu Lys Ser 1 5 10
- Glu Leu Lys Arg Arg Asn Leu Asp Ile Thr Gly Val Lys Thr Val Leu 15 20 25

Ile Ser Arg Leu Arg
30

- 12) INFORMATION FOR SEQ ID NO: 507:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 137 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (11) MOLECULE TYPE: PROTEIN
 - .vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - F) TISSUE TYPE: kidney
 - .ik FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -17..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.2

seq SLLXRVSVTAVAA/LS

-15

-10

_

Ala Leu Ser Gly Arg Pro Leu Gly Thr Xaa Leu Gly Phe Gly Gly Phe 1 5 10 15

Leu Thr Arg Gly Phe Pro Lys Ala Ala Ala Pro Val Arg His Ser Gly 20 25 30

Asp His Gly Lys Arg Leu Phe Val Ile Arg Pro Ser Arg Phe Tyr Asp 35 40 45

Arg Arg Phe Leu Lys Leu Leu Arg Phe Tyr Ile Ala Leu Thr Gly Ile 50 60 .

Pro Val Ala Xaa Phe Ile Thr Leu Val Asn Val Phe Ile Gly Gln Ala 65 70 75

Glu Leu Ala Glu Ile Pro Glu Gly Tyr Val Pro Glu His Trp Glu Tyr 80 95

Tyr Lys His Pro Ile Ser Arg Trp Ile Ala Arg Asn Phe Tyr Asp Ser 100 105 110

Pro Xaa Lys Ile Tyr Glu Arg Thr Met 115 120

(2) INFORMATION FOR SEQ ID NO: 508:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Lymph ganglia
- (ix) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -25..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.2 seg LDLLRGLPRVSLA/NL
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508:

Met Ala Gly Pro Leu Gln Gly Gly Gly Ala Arg Ala Leu Asp Leu Leu -25 -15 -10

Arg Gly Leu Pro Arg Val Ser Leu Ala Asn Leu Lys Pro Asn Pro Gly
-5 1 5

Ser Lys Lys Pro Glu Arg Arg Pro Arg Gly Arg Arg Gly Arg Lys
10 15 20

Cys Gly Arg Gly His Lys Gly Glu Arg Gln Arg Gly Thr Arg Pro Arg

35

25

Leu Gly Phe Glu Gly Gly Gln Thr Pro Phe Tyr Ile Arg Xaa Pro Lys 40 50 55

30

Tyr Gly Phe Asn Glu Gly His Ser Phe Arg Arg Gln Tyr Lys Pro Leu 60 65 70

Ser Leu Asn Arg Leu Gln Tyr Leu Ile Asp Leu Gly Arg Val Asp Pro 75 80 85

Ser Gln Pro Ile Asp Leu Thr Gln Leu Val Asn Gly Arg Gly Val Thr 90 95 100

Ile Ala Pro 105

(2) INFORMATION FOR SEQ ID NO: 509:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 136 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (V1) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -41..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.1

seq GILILWIIRLLFS/KT

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509:
- Met Ala Thr Ala Thr Glu Gln Trp Val Leu Val Glu Met Val Gln Ala
 -40 -35 -30
- 1-1 Tyr Gir Ala Pro Ala Tyr His Leu Ile Leu Glu Gly Ile Leu Ile -20 -15 -10
- Let Trp Ile Ile Arg Leu Leu Phe Ser Lys Thr Tyr Lys Leu Gln Glu -5 5
- Ang Ser Asp Leu Thr Val Lys Glu Lys Glu Glu Leu Ile Glu Glu Trp
- on and the Fro Leu Val Pro Pro Val Pro Lys Asp His Pro Ala Leu

Gly Lys Glu Cys Ile Asn Phe Ala Ser Phe Asn Phe Leu Gly Leu Leu 60 65 70

Asp Asn Pro Arg Val Lys Ala Ala Leu Ala Ser Leu Lys Lys Tyr
75 80 85

Gly Val Gly Thr Cys Gly Pro Cys 90 95

- (2) INFORMATION FOR SEQ ID NO: 510:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Substantia nigra
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -79..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.1

seq QGVLFICFTCARS/FP

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510:
- Met Glu Asp Pro Asn Pro Glu Glu Asn Met Xaa Gln Gln Asp Ser Pro
 -75 -70 -65
- Lys Glu Arg Ser Pro Gln Ser Pro Gly Gly Asn Ile Cys His Leu Gly
 -60 -55 -50
- Ala Pro Lys Cys Thr Arg Cys Leu Ile Thr Phe Ala Asp Ser Lys Xaa -45 -35
- Xaa Glu Arg His Met Lys Arg Glu His Pro Ala Asp Phe Val Ala Gln
 -30 -25 -20
- Lys Leu Gln Gly Val Leu Phe Ile Cys Phe Thr Cys Ala Arg Ser Phe -15 -10 -5 1

Pro Ser

- (2) INFORMATION FOR SEQ ID NO: 511:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 142 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -32..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.1

seq RLLSSLLLTMSNN/NP

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511:
- Met Asn Val Ile Asp His Val Arg Asp Met Ala Ala Gly Leu His -30 -25 -20
- Ser Asn Val Arg Leu Leu Ser Ser Leu Leu Leu Thr Met Ser Asn Asn -15 -5
- Asn Pro Glu Leu Phe Ser Pro Pro Gln Lys Tyr Gln Leu Leu Val Tyr

 1 10 15
- His Ala Asp Ser Leu Phe His Asp Lys Glu Tyr Arg Asn Ala Val Ser 20 25 30
- Lys Tyr Thr Met Ala Leu Gln Gln Lys Lys Ala Leu Ser Lys Thr Ser 35 40 45
- Lys Val Arg Pro Ser Thr Gly Asn Ser Ala Ser Thr Pro Gln Ser Gln 50 55 60
- Cys Leu Pro Ser Glu Ile Glu Val Lys Tyr Lys Met Ala Glu Cys Tyr 65 70 75 80
- Thr Met Leu Lys Gln Asp Lys Asp Ala Ile Ala Ile Leu Asp Gly Xaa 85 90 95

Charles are a second at a term of the first

- Pro Phe Lys Thr Lys Asn Ser Gln Asn Lys His Asp Ala Gly 100 105 110
- 125 INFORMATION FOR SEQ ID NO: 512:
 - (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain

(D) OTHER INFORMATION: score 4.1

seg LVHHCPTWQWATG/EE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512:

Met Gln Asn Val Ile Asn Thr Val Lys Gly Lys Ala Leu Glu Val Ala
-55 -50 -45

Glu Tyr Leu Thr Pro Val Leu Lys Glu Ser Lys Phe Lys Glu Thr Gly
-40 -35 -30

Val Ile Thr Pro Glu Glu Phe Val Ala Ala Gly Asp His Leu Val His -25 -15

His Cys Pro Thr Trp Gln Trp Ala Thr Gly Glu Glu Leu Lys Val Lys -10 -5 1 5

Ala Tyr Leu Pro Thr Gly Lys Trp

(2) INFORMATION FOR SEQ ID NO: 513:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 91 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Colon
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -88..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.1 seq CIQRLPWLLLCRG/IT
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513:

Met Ala Thr Leu Thr Phe Ser Leu Arg Lys Pro Leu Gln Arg Ser Leu -85 -75

Ile Arg Pro Ser His Leu Pro Leu Cys Cys Phe Asp Trp Arg Leu Ser
-70 -65 -60

His Tyr Tyr Arg Leu Pro Pro Ala Val Arg Leu His Gln Gln Arg Gly -55 -50 -45

Gly Arg Pro Gly Arg Ser Ser Ala Asp His Trp His Ser Gly Val Pro
-40 -35 -30 -25

Thr Arg Ile Leu Pro Pro Ala His Arg Leu Leu Cys Ile Gln Arg Leu
-20 -15 -10

Pro Trp Leu Leu Cys Arg Gly Ile Thr Ser
-5

- .2 INFORMATION FOR SEQ ID NO: 514:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (11) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -49..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4 seq PSLAAGLLFGSXA/GL
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514:
- Met Glu Lys Pro Leu Phe Pro Leu Val Pro Leu His Trp Phe Gly Phe
 -45
 -35
- Gly Tyr Thr Ala Leu Val Val Ser Gly Gly Ile Val Gly Tyr Val Lys
 -30 -25 -20
- Thr Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Xaa -15 -5
- Ala Gly Leu Gly Ala Tyr Gln Leu Tyr Gln Asp Pro Arg Asn Val Trp
 1 5 10 15
- Gly Phe Leu Ala Ala Thr Ser Val 20
- ..: INFORMATION FOR SEQ ID NO: 515:
 - (1) SETUENCE CHARACTERISTICS:
 - (A) LENGTH: 65 amino acids
 - THE TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (11' MOLECULE TYPE: PROTEIN
 - www. CRIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens

- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4 seq VAVGLTIAAAGFA/GR
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515:

Met Ala Ser Thr Val Val Ala Val Gly Leu Thr Ile Ala Ala Gly -15 -10 -5

Val Lys Gln Val Phe Gln Ser Leu Pro Lys Ser Ala Phe Ser Gly Gly
15 20 25 30

Tyr Tyr Arg Gly Xaa Phe Glu Pro Xaa Met Xaa Lys Arg Glu Ala Ala 35 40 45

Gly

- (2) INFORMATION FOR SEQ ID NO: 516:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 110 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -83..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4 seq AFSFSRLLSQCRP/DC
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516:

Met Val Ile Arg Val Tyr Ile Ala Ser Ser Ser Gly Ser Thr Ala Ile
-90 -75 -70

Lys Lys Gln Gln Asp Val Leu Gly Phe Leu Glu Ala Asn Lys Ile
-65 -60 -55

Sly Phe Glu Slu Lys Asp Ile Ala Ala Asn Glu Glu Asn Arg Lys Trp -50 -45 -40

Met Arg Glu Asn Val Pro Glu Asn Ser Arg Pro Ala Val Gln Gly Pro -35 -25 -20

His Ala Phe Arg Tyr Lys Ala Phe Ser Phe Ser Arg Leu Leu Ser Gln
-15 -10 -5

Cys Arg Pro Asp Cys Leu Asn Met Leu Arg Arg Phe Ser Gln Tyr Cys

1 10

Let Tyr Let Val Met Glu Lys Ala Let Let Phe Phe Phe 15 20 25

- (2) INFORMATION FOR SEQ ID NO: 517:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (11) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -42..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4

seq ITSSLFLGRGSVA/SN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517:

Met Ser Ser Arg Gly His Ser Thr Leu Pro Arg Thr Leu Met Ala Pro
-40 -35 -30

Arg Met Ile Ser Glu Gly Asp Ile Gly Gly Ile Ala Gln Ile Thr Ser -25 -20 -15

Ser Leu Phe Leu Gly Arg Gly Ser Val Ala Ser Asn Arg His Leu Leu -10 -5 1 5

Cln Ala Arg Gly Ile 10

INFORMATION FOR SEQ ID NO: 518:

1 DEQUENCE CHARACTERISTICS:

A) LENGTH: 55 amino acids

[B] TYPE: AMING ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

vi ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9

seq PALCLFDVDGTLT/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518:

Met Ala Ala Pro Gly Pro Ala Leu Cys Leu Phe Asp Val Asp Gly Thr -15 -10 -5

Leu Thr Ala Pro Arg Gln Lys Ile Thr Lys Glu Met Asp Asp Phe Leu
1 5 10

Gln Lys Leu Arg Gln Lys Ile Lys Ile Gly Val Val Gly Gly Ser Asp 15 20 25 30

Phe Glu Lys Val Gln Glu Arg

- (2) INFORMATION FOR SEQ ID NO: 519:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Normal prostate
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -19..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 3.9

sec ILFHGVFYAGGFA/IV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519:

Met Pro Leu Gly Ala Arg Ile Leu Phe His Gly Val Phe Tyr Ala Gly -15 -10 -5

Gly Phe Ala Ile Val Tyr Tyr Leu Ile Gln Lys Phe His Ser Arg Thr
1 5 10

Leu

- (2) INFORMATION FOR SEQ ID NO: 520:
 - (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR

- (ii) MOLECULE TYPE: PROTEIN
- (v1) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Cancerous prostate
- (1x) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -13..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 3.9

seq MLLSIGMLMLSAT/QV

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 520:

Met Leu Ser Ile Gly Met Leu Met Leu Ser Ala Thr Gln Val Tyr
-10 -5 1

Thr Ile Leu Thr Val Gln Leu Phe Ala Phe Leu Asn Leu Leu Pro Val 5 10 15

Glu Xaa Asp Ile Leu Ala Tyr Asn Phe Glu Asn Ala Ser Gln Thr Phe 20 25 30 35

Asp Asp Leu Pro Ala Arg Phe Gly Tyr
40

- (2) INFORMATION FOR SEQ ID NO: 521:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (11) MOLECULE TYPE: PROTEIN
 - (v1) OSIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Uterus
 - (1M) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (3) LOCATION: -25..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 3.9

seq WIAAVTIAAGTAA/IG

- (M1) SEQUENCE DESCRIPTION: SEQ ID NO: 521:
- Met Ser Led Thr Ser Ser Ser Ser Val Arg Val Glu Trp Ile Ala Ala -... -15 -15

Ile Gln Lys Asp Asn Pro Lys Ile Val His Ala Phe Asp Met Glu Asp 25 30 35

Xaa Xaa Asp Lys Ala Val Tyr Cys Arg Cys Trp Arg Ser Lys Lys Phe 40 45 50 55

Pro Phe Cys Asp Gly Ala His Thr Xaa Xaa Asn Glu Glu Thr Gly Leu 60 65 70

(2) INFORMATION FOR SEQ ID NO: 522:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 108 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Cancerous prostate
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -61..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 3.9 seq YTAVSVLAGPRWA/DP
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522:

Met Ser Gly Ser Asn Gly Ser Lys Glu Asn Ser His Asn Lys Ala Arg
-60 -55

Thr Ser Pro Tyr Pro Gly Ser Lys Val Glu Arg Ser Gln Val Pro Asn
-45 -35 -30

Glu Lys Val Gly Trp Leu Val Glu Trp Gln Asp Tyr Lys Pro Val Glu
-25 -20 -15

Tyr Thr Ala Val Ser Val Leu Ala Gly Pro Arg Trp Ala Asp Pro Gln
-10 -5 1

Ile Ser Xaa Ser Xaa Phe Ser Pro Lys Phe Asn Glu Lys Asp Gly His
5 10 15

Val Glu Arg Xaa Ser Lys Asn Gly Leu Tyr Glu Ile Xaa Asn Gly Arg 20 25 30 35

Pro Arg Asn Pro Ala Asp Gly Leu Asp Trp Trp Ala 40 45

- (2) INFORMATION FOR SEQ ID NO: 523:
 - (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Cancerous prostate
- (1K) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -30..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 3.9

seq LWMRWTVTSTTRA/WI

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 523:

Met Ala Ile Ser Leu Arg Ser Ser Gly Ile Ser Val Lys Cys Leu Ser -30 -25 -20 -15

Lys Leu Trp Met Arg Trp Thr Val Thr Ser Thr Thr Arg Ala Trp Ile
-10 -5 1

Xaa Ala Glu Pro Pro Gln Leu Asp Ile Ser 5 10

- (2) INFORMATION FOR SEQ ID NO: 524:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 65 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Uterus
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -27..-1
 - (3) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 3.8

seg FVLGSARLGGSGS/MR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524:

Det ser Gl. Val Arg Leu Pro Pro Leu Arg Ala Leu Asp Asp The Val -20 -15 10

15

20

Pro Ser Leu Leu Arg His Arg Pro Arg Ser Arg Arg Val Arg Thr Ala 25 30 35

Thr

- (2) INFORMATION FOR SEQ ID NO: 525:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Muscle
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -15..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 3.8

seq LVSATAWLEECWW/SE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525:

Met Lys Leu Val Ser Ala Thr Ala Trp Leu Glu Glu Cys Trp Trp Ser -15 -5 1

Glu Leu Ser

- (2) INFORMATION FOR SEQ ID NO: 526:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -34..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 3.8

seq LYVPLLAVCCLHS/VV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526:

Met Lys Ala Ile Ser Val Ser Leu Leu Arg Leu Thr Lys Leu Leu Trp
-30 -25 -20

Phe Phe Ser Ile Val Leu Tyr Val Pro Leu Leu Ala Val Cys Cys Leu
-15 -10 -5

His Ser Val Val Phe Phe

(2) INFORMATION FOR SEQ ID NO: 527:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 143 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (11) MOLECULE TYPE: PROTEIN
- (V1) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Thyroid
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -118..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 3.8 seq LMIALTVVGCIFM/VI
- (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 527:

Met Gly Ser Leu Ser Gly Leu Arg Leu Ala Ala Gly Ser Cys Phe Arg
-115 -110 -105

Leu Cys Glu Arg Asp Val Ser Xaa Ser Leu Arg Leu Thr Arg Ser Ser
-100 -95 -90

Asp Leu Lys Arg Ile Asn Gly Phe Cys Thr Lys Pro Gln Glu Ser Pro -85 -80 -75

Gly Ala Pro Ser Arg Thr Tyr Asn Arg Val Pro Leu His Lys Pro Thr
-T -65 -60 -55

Add Trp Gln Lys Lys Ile Leu Ile Trp Ser Gly Arg Phe Lys Lys Glu -50 -45

Ela Eau Ile Pro Glu Thr Val Ser Leu Glu Met Leu Xaa Xaa Ala Lys -35 +30 +25

Act Tys Met Arg Val Lys Ile Ser Tyr Leu Met Ile Ala Leu Thr Val

- (2) INFORMATION FOR SEQ ID NO: 528:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 118 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -100..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 3.7

seq LASSFLFTMGGLG/FI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528:

Met Glu Thr Leu Tyr Arg Val Pro Phe Leu Val Leu Glu Cys Pro Asn -100 -95 -90 -85

Leu Lys Leu Lys Pro Pro Trp Leu His Met Pro Ser Ala Met Thr
-80 -75 -70

Val Tyr Ala Leu Val Val Val Ser Tyr Phe Leu Ile Thr Gly Gly Ile
-65 -60 -55

Ile Tyr Asp Val Ile Val Glu Pro Pro Ser Val Gly Ser Met Thr Asp
-50
-45

Glu His Gly His Gln Arg Pro Val Ala Phe Leu Ala Tyr Arg Val Asn
-35
-25

Gly Gln Tyr Ile Met Glu Gly Leu Ala Ser Ser Phe Leu Phe Thr Met -20 -15 -10 -5

Gly Gly Leu Gly Phe Ile Ile Leu Asp Gly Ser Xaa Ala Pro Asn Ile 1 5 10

Pro Lys Leu Asn Arg Phe 15

- (2) INFORMATION FOR SEQ ID NO: 529:
 - (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Cancerous prostate
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -13..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 3.7

seq MLVLRSGLTKALA/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529:

Met Leu Val Leu Arg Ser Gly Leu Thr Lys Ala Leu Ala Ser Arg Thr
-10 -5 1

Leu Ala Xaa Gln Xaa Xaa Phe Ala His Arg Ala Glu Val Arg Lys Ala 5 10 15

Leu Ala Asn Cys Lys Glu Trp Gln Glu Gln Ser Ile Ile Pro Asn Leu 20 25 30 35

Ala Arg Ile Asp Lys Gln Glu Thr Arg
40

- (2) INFORMATION FOR SEQ ID NO: 530:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (11) MOLECULE TYPE: PROTEIN
 - (v1) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Thyroid
 - (1x) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -36..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 3.7

seq NIESLAWTGGTLG/HP

- .x:/ SEQUENCE DESCRIPTION: SEQ ID NO: 530:
- INt Ala Ala Pro Leu Ser Val Glu Val Glu Phe Gly Gly Gly Ala Xaa -35 -25
- Fig. 170 170 Thr Val Leu Arg Ash Ile Glu Ser Leu Ala Trp Thr Gly -15 -10

25

15

Arg Asn Ser Gly Ala Asp Tyr Arg

(2) INFORMATION FOR SEQ ID NO: 531:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Umbilical cord
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -65..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 3.7

seq FVGGLPVIFWSWA/GL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531:

Met Thr His Leu Ile Glu Tyr Asp Arg His Arg Lys Ser Arg Leu Ser
-65 -50 -55

Pro Leu Gln His Leu Tyr Leu Leu Pro Ala Asp His Ser Arg Asn Ala
-45
-40
-35

Ala Glu Arg Phe Pro Gly Ala Trp Phe Gln Pro Pro Thr Val Asp Ser
-30 -25 -20

Glu Ala Ser Ala Phe Val Gly Gly Leu Pro Val Ile Phe Trp Ser Trp
-15 -10 -5

Ala Gly Leu Val

- (2) INFORMATION FOR SEQ ID NO: 532:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 104 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Uterus
 - (ix) FERTURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7

seq WARKLLSVPWLLC/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532:

Met Ala Ala Ala Leu Gly Gln Ile Trp Ala Arg Lys Leu Leu Ser -20 -15 -10

Val Pro Trp Leu Leu Cys Gly Pro Arg Arg Tyr Ala Ser Ser Phe
-5 1 5 10

Lys Ala Ala Asp Leu Gln Leu Glu Met Thr Gln Lys Pro His Lys Lys
15 20 25

Pro Gly Pro Gly Glu Pro Leu Val Phe Gly Lys Thr Phe Thr Asp His 30 35 40

Met Leu Met Val Glu Trp Asn Asp Lys Gly Trp Gly Gln Pro Arg Ile
45 50 55

Gln Pro Phe Gln Asn Leu Thr Leu His Pro Ala Ser Ser Ser Leu His
60 65 70

Tyr Ser Leu Gln Leu Phe Glu Gly 75 80

(2) INFORMATION FOR SEQ ID NO: 533:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (11) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Hypertrophic prostate
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - [8] LOCATION: -38..-1
 - 13 IDENTIFICATION METHOD: Von Heigne matrix
 - (0) OTHER INFORMATION: score 3.7

seq CPLLLLVFTTNNG/RH

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533:
- Ser Ala Mai Mid Ser Arg Val Thr Gln Glu Glu Ile Lys Lys Glu Pro

Phe Thr Thr Asn Asn Gly Arg His His Arg Met Asp Glu Phe Ser Arg -5 10

Gly Asn Val Pro Ser Ser Glu Leu Gln Ile Tyr Thr Trp Met Asp Ala •15 20 25

Thr Leu Lys Glu Leu Thr Ser Leu Val Lys Glu Val Tyr Pro Glu Ala 30 35 40

Arg Xaa Lys Gly Thr His Phe Asn Phe Ala Xaa Val Phe Thr Asp Val
45 50 55

Lys Arg Pro 60

- (2) INFORMATION FOR SEQ ID NO: 534:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -22..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 3.7 seq AVLDCAFYDPTHA/WS
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534:

Met Arg Leu Lys Tyr Gln His Thr Gly Ala Val Leu Asp Cys Ala Phe -20 -15 -10

Tyr Asp Pro Thr His Ala Trp Ser Gly Gly Leu Asp His Gln Leu Lys
-5 1 5 10

Met His Asp Leu Asn Thr Asp Gln Glu Asn Leu Val Gly Thr Met Met 15 20 25

Pro Leu Ser Asp Val Leu 30

- (2) INFORMATION FOR SEQ ID NO: 535:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 88 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR

- (ii) MCLECULE TYPE: PROTEIN
- (v1) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Uterus
- (ix) FEATURE:
 - (A) NAME/KEY: sig peptide
 - (B) LOCATION: -86..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 3.7

seq WAVVLADTAVTSG/RG

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535:
- Met Ala Leu Leu Phe Ala Arg Ser Leu Arg Leu Cys Arg Trp Gly Ala
 -85
 -75
- Lys Arg Leu Gly Val Ala Ser Thr Glu Ala Gln Arg Gly Val Ser Phe
 -70 -65 -60 -55
- Lys Leo Xaa Glu Lys Thr Ala His Ser Ser Leo Ala Leo Phe Arg Asp
 -50 -45 -40
- Asp Thr Gly Val Lys Tyr Gly Leu Val Gly Leu Glu Pro Thr Lys Val -35 -30 -25
- Ala Leu Asn Val Glu Arg Phe Arg Glu Trp Ala Val Val Leu Ala Asp
 -20 -15 -10

Thr Ala Val Thr Ser Gly Arg Gly

- (2) INFORMATION FOR SEQ ID NO: 536:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MGLECULE TYPE: PROTEIN
 - (vi) GRIGINAL SOURCE:
 - Al ORGANISM: Homo Sapiens
 - F) TISSUE TYPE: Umbilical cord
 - (1x) FEATURE:
 - (a) NAME/KEY: sig_peptide
 - (B) LOCATION: -68..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (C) OTHER INFORMATION: score 3.6

seq ILLGNYCVAVADA/KK

-65

-60

-55

Ser Phe Ser Asp Ala Leu Ile Asp Glu Asp Pro Gln Ala Ala Leu Glu
-50 -45 -40

Glu Leu Thr Lys Ala Leu Glu Gln Lys Pro Asp Asp Ala Gln Tyr Tyr
-35 -30 -25

Cys Gln Arg Ala Tyr Cys His Ile Leu Leu Gly Asn Tyr Cys Val Ala
-20 -15 -10 -5

Val Ala Asp Ala Lys Lys Ser Leu Glu Leu Asn Pro Asn Asn Ser Thr
1 5 10

Ala Met Leu Arg Lys Gly Ile Cys Glu Tyr His Glu Lys Asn Tyr Ala 15 20 25

Ala Ala Leu Glu Thr Phe Tyr Arg Arg Thr Gly 30 35

(2) INFORMATION FOR SEQ ID NO: 537:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 81 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -60..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 3.5 seq WFYIGSSLNGTRG/KR
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537:

Met Ala Gln Leu Lys Tyr Met Glu Asn Val Gly Tyr Ala Gln Glu Asp
-60 -55 -50 -45

Arg Glu Arg Met His Arg Asn Ile Val Ser Leu Ala Gln Asn Leu Leu
-40 -35 -30

Asn Phe Met Ile Gly Ser Ile Leu Asp Leu Trp Gln Cys Phe Leu Trp -25 -15

Phe Tyr Ile Gly Ser Ser Leu Asn Gly Thr Arg Gly Lys Arg Val Pro-

Ala His Phe Ser Asn Thr Ser Leu His Tyr Leu Asn Ala Ala Trp Pro
5 10 15 20

- (2) INFORMATION FOR SEQ ID NO: 538:
 - (I) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 amino acids
 - (B) TYPE: AMINO ACID
 - (1) TOPOLOGY: LINEAR
 - (11) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Brain
 - (1x) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (P) LOCATION: -31..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix

661

- (E) OTHER INFORMATION: score 3.5 seq WSPLSTRSGGTHA/CS
- (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 538:
- Met Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly -30 -25
- Ser Phe Trp Ser Pro Leu Ser Thr Arg Ser Gly Gly Thr His Ala Cys -15 -10

Ser Ala Ser Met Arg Gln Pro Trp

- (2) INFORMATION FOR SEQ ID NO: 539:
 - (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 110 amino acids
 - (3) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - ::: MOLECULE TYPE: PROTEIN
 - TI ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - [3] TISSUE TYPE: Substantia nigra
 - Tix, FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (8) LOCATION: -54..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - OF OTHER INFORMATION: score 3.5

Met Ala Asp Glu Glu Leu Glu Ala Leu Arg Arg Gln Arg Leu Ala Glu
-50 -45 -40

Leu Gln Ala Lys His Gly Asp Pro Gly Asp Ala Ala Gln Gln Glu Ala
-35
-30
-25

Lys His Arg Glu Ala Glu Met Arg Asn Ser Ile Leu Ala Gl
n Val Leu -20 -15 -10

Asp Gln Ser Ala Arg Ala Arg Leu Ser Asn Leu Ala Leu Val Lys Pro
-5 1 5 10

Glu Lys Thr Lys Ala Val Glu Asn Tyr Leu Ile Gln Met Ala Arg Tyr
15 20 25

Gly Gln Leu Ser Glu Lys Val Ser Glu Gln Gly Leu Ile Glu Ile Leu 30 35 40

Lys Lys Val Ser Gln Gln Thr Glu Lys Xaa Thr Thr Val Arg
45 50 55

(2) INFORMATION FOR SEO ID NO: 540:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 86 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Cancerous prostate
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -63..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 3.5

seq GLVCAGLADMARP/AE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540:

Met Ser Ala Ala Gly Ala Arg Gly Leu Arg Ala Thr Tyr His Arg Leu
-60 -55 -50

Leu Asp Lys Val Glu Leu Met Leu Pro Glu Lys Leu Arg Pro Leu Tyr
-45 -40 -35

Asn His Pro Ala Gly Pro Arg Thr Val Phe Phe Trp Ala Pro Ile Met -30 -25 -20

Lys Trp Gly Leu Val Cys Ala Gly Leu Ala Asp Met Ala Arg Pro Ala -15 -5 1

Glu Lys Leu Ser Thr Ala Gln Ser Xaa Val Leu Met Ala Thr Gly Phe
5 10 15

Ile Trp Ser Arg Tyr Ser 20

- (2) INFORMATION FOR SEQ ID NO: 541:
 - (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 127 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (11) MOLECULE TYPE: PROTEIN
 - (V1) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Muscle
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -86..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 3.5

seq TGXLNMTLQRASA/AP

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541:
- Met Ser Asn Tyr Ser Val Ser Leu Val Gly Pro Ala Pro Trp Gly Phe
 -85 -80 -75
- Arg Leu Gln Gly Gly Lys Asp Phe Asn Met Pro Leu Thr Ile Ser Ser -70 -65 -60 -55
- Leu Lys Asp Gly Gly Lys Ala Ala Gln Ala Asn Val Arg Ile Gly Asp
 -50 -45 -40
- Val Val Leu Ser Ile Asp Gly Ile Asn Ala Gln Gly Met Thr His Leu
 -35 -30 -25
- Glu Ala Gln Asn Lys Ile Lys Gly Cys Thr Gly Xaa Leu Asn Met Thr -20 -15 -10
- Leu Gln Arg Ala Ser Ala Ala Pro Lys Pro Glu Pro Val Pro Val Gln
- Lys Pro Thr Val Thr Ser Val Cys Ser Glu Thr Ser Gln Glu Leu Ala
 15 20 25
- Glu Gly Gln Arg Arg Gly Ser Gln Gly Asp Ser Lys Gln Gln Asn 30 35 40
- 10" INFORMATION FOR SEQ ID NO: 542:

The region of the particle of the con-

- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Uterus
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -18..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 3.5

seq LLGLELSEAEAIG/AD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542:

Met Ala Asn Pro Lys Leu Leu Gly Leu Glu Leu Ser Glu Ala Glu Ala -15 -5

Ile Gly Ala Asp Ser Ala Arg Phe Glu Glu Leu Leu Gln Ala Ser 1 5 10

Lys Glu Leu Gln Gln

- (2) INFORMATION FOR SEQ ID NO: 543:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: brain
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -40..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 3.5

seq ALLCTLLLHFQNI/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543:

Met Ile Ile Pro Leu Leu Glu Ile Leu Ile Ile Ile Val Leu Asn Glu -40 -35 -30 -25

Val Leu Phe Asp Val Asn Ser Val Tyr Lys Ala Leu Leu Cys Thr
-20 -15 -10

Leu Leu His Phe Gln Asn Ile Arg Arg Phe Leu Ser Ser Gln Ser +5 1 5

Pro Met Lys Ala Val Ser Leu Leu Xaa Phe His Gln Pro Asp Phe Asp

20

10

Tyr Ile 25

(2) INFORMATION FOR SEQ ID NO: 544:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids

15

- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR
- (i1) MOLECULE TYPE: PROTEIN
- (V1) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Lymph ganglia
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -52..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 7.4

seq LVFIIGLVGNLLA/LV

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544:
- Met Asp Ile Gln Met Ala Asn Asn Phe Thr Pro Pro Ser Ala Thr Pro
 -50 -45 -40
- Gln Gly Asn Asp Cys Asp Leu Tyr Ala His His Ser Thr Ala Arg Ile
 -35
 -25
- Val Met Pro Leu His Tyr Ser Leu Val Phe Ile Ile Gly Leu Val Gly -20 -15 -10 -5
- Ash Leu Leu Ala Leu Val Val Ile Val Gln Ash Arg Lys Lys Ile Ash
 1 5 10
- Ser Thr Thr Leu Tyr Ser Thr Asn Leu Val Ile Ser Asp Ile Leu Phe
 15 20 25
- The Thr Ala Leu Pro Thr Arg Ile Ala Thr Met Xaa Trp Ala Leu Thr 30 40
- il old For Glu Met Trp
- 1. INFORMATION FOR SEQ ID NO: 545:
 - 1 SEQUENCE CHARACTERISTICS:

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Pancreas
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -29..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 7 seq SMIGIGSLPSCWA/CW
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545:

Met Leu Thr Ile Val Lys Ser Pro Gln Lys Ser Tyr Leu Phe Pro Ser -25 -20 -15

Ser Met Ile Gly Ile Gly Ser Leu Pro Ser Cys Trp Ala Cys Trp Ile -10 -5 1

Gln Gln Arg 5